

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:12:53 ; Search time 29.96 Seconds
(without alignments)
37.074 Million cell updates/sec

Title: US-09-724-842-27
Perfect score: 55
Sequence: 1 HHQKLVFFAQ 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	22	AA82641
2	55	100.0	28	17	AAW01414
3	55	100.0	28	22	AA835600
4	55	100.0	35	22	AA891803
5	55	100.0	35	22	AA891830
6	55	100.0	40	19	AAW47232
7	55	100.0	53	15	AAW55697
8	55	100.0	63	18	AAW26511
9	55	100.0	63	18	AAW26391
10	55	100.0	63	19	AAW44746
11	55	100.0	63	19	AAW42975

12	55	100.0	99	16	AA874695
13	52	94.5	10	22	AA846225
14	52	94.5	15	20	AAW89358
15	52	94.5	17	15	AAW54703
16	52	94.5	17	22	AA891774
17	52	94.5	17	22	AA891807
18	52	94.5	17	22	AA848346
19	52	94.5	18	21	AA810963
20	52	94.5	19	18	AAW18882
21	52	94.5	19	18	AAW18881
22	52	94.5	19	22	AA846201
23	52	94.5	19	22	AA849097
24	52	94.5	21	20	AA830941
25	52	94.5	24	15	AAW52569
26	52	94.5	26	19	AAW47229
27	52	94.5	26	20	AAW33408
28	52	94.5	27	20	AAW33409
29	52	94.5	28	8	AAW70594
30	52	94.5	28	10	AAW90381
31	52	94.5	28	15	AAW54702
32	52	94.5	28	15	AAW60368
33	52	94.5	28	16	AAW64170
34	52	94.5	28	16	AAW64171
35	52	94.5	28	16	AAW64172
36	52	94.5	28	17	AAW01413
37	52	94.5	28	17	AAW01413
38	52	94.5	28	20	AAW39805
39	52	94.5	28	20	AAW81467
40	52	94.5	28	22	AAW91783
41	52	94.5	28	22	AAW91789
42	52	94.5	28	22	AAW91800
43	52	94.5	28	22	AAW91816
44	52	94.5	28	22	AAW91827
45	52	94.5	28	22	AAW49396

ALIGNMENTS

RESULT 1
AA82641
ID AA82641 standard; Peptide: 10 AA.
XX
AC AA82641;
XX
DT 02-OCR-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease;
KW vaccine; therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..10 /note= "all D-form residues"
FT
XX
PN WO200139796-A2.
XX
PD 07-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-CA01413.
XX
PR 29-NOV-1999; 99US-0168594.
XX
PR 28-NOV-2000; 2000US-0724842.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Chalifour R, Hebert L, Kong X, Gervais F;
XX
DR WPI; 2001-441458/47.
XX

Beta-amyloid precu
Human APP derived
Beta-amyloid pept1
Beta-amyloid fragm
Amyloid beta-prote
Amyloid beta-prote
Beta-amyloid antig
Beta-amyloid precu
AEDANS-beta-amyloi
Trp-Beta-amyloid p
Human APP A-beta 1
Human amyloid beta
Human secretase SE
Alzheimer's disease
Beta-amyloid pept1
Human amyloidogeni
Human amyloidogeni
Sequence of Alzhei
Synthetic A4 amylo
Beta-amyloid fragm
Beta-amyloid (1-28
A4-O(1-28) a parti
A4-P(1-28) a parti
A4-B(1-28) a parti
Generic beta amylo
Beta/A4-amyloid pe
Beta-amyloid prote
Synthetic amyloid
Amyloid beta-prote
Amyloid beta-prote
Amyloid beta-prote
Amyloid beta-prote
Human amyloid pept

PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, e.g. as
 PT vaccine, which elicits production of antibodies to prevent
 PT fibrillogenesis and associated cellular toxicity -
 XX
 XX
 PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for
 CC use in preparing vaccines for preventing or treating Alzheimer's
 CC disease and other amyloid related disorders in humans. It is based
 CC on a portion of amyloid-beta peptide (see AAB82622), and may be
 CC modified by removing or inserting 1 or more amino acid residues, or
 CC by substituting 1 or more amino acid residues with other amino acid
 CC residues or non-amino acid fragments. Vaccines of the invention
 CC are produced using 'non-self' peptides synthesised from the
 CC unnatural D-configuration amino acids to avoid the drawbacks of
 CC 'self' proteins. The all-D peptides need not be aggregated to be
 CC operative or immunogenic. They preferably interact with at
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region
 CC or GAG-binding site region, the amyloid-beta peptide, or their
 CC immunogenic fragments, protein conjugates, immunogenic derivative
 CC peptides and immunogenic peptidomimetics. Examples include all-D
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
 CC 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
 CC derivative peptides given in AAB82623-64. The vaccine elicits a
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and
 CC associated cellular toxicity. The amyloid related diseases may be
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein
 CC related disorders, or systemic amyloidosis associated with chronic
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and
 CC systemic amyloidosis found in long-term haemodialysis patients.
 XX
 XX

Sequence 10 AA;

Query Match 100.0%; Score 55; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 Db 1 hhqklvffaq 10

RESULT 2

ID AAW01414 standard; Protein; 28 AA.
 XX
 AC AAW01414;

DT 20-JAN-1997 (first entry)

DE Beta/A4-amyloid peptide residues 1-28 Dutch.

XX Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;
 KW Alzheimer's disease; stimulation; investigation; pathogenesis;
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;
 KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
 KW hemorrhage.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 22

FT /note- "wild type Glu substd. with Gln"

XX W09615799-A1.

XX 30-MAY-1996.

XX

PF 22-NOV-1995; 9SWO-US15007.
 PR 22-NOV-1994; 94US-0347144.
 XX
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Anderson S;

DR WPI; 1996-268332/27.

XX Use of agents which bind beta-amyloid peptide - for diagnosis,
 PT prevention and treatment of vascular damage caused by amyloid
 PT deposits, partic. in haemorrhaging and Alzheimer's disease
 XX
 PS Example 1; Fig 1; 52pp; English.

XX To investigate the effects of beta-amyloid peptide (BAP) on
 CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
 CC One peptide contained 42 amino acids and corresp. to the full
 CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
 CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
 CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
 CC (HCHWA-D), respectively. In an assay to determine the effect of
 CC the peptides on t-PA activation, each peptide (AAR95248, 49 and 50)
 CC gave 1st order rate constant of activation (k(app)) values of
 CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
 CC and fibrinogen controls. The results demonstrate that the BAP are
 CC able to stimulate t-PA activity in vitro, which is significant in
 CC that it provides a means for investigating and controlling the
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
 CC angiopathy related cerebral haemorrhage.

XX Sequence 28 AA;

Query Match 100.0%; Score 55; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 Db 13 hhqklvffaq 22

RESULT 3

AAB35600
 ID AAB35600 standard; peptide; 28 AA.
 XX
 AC AAB35600;

DT 15-FEB-2001 (first entry)

DE Human clone E22Q B(1-28) amyloid B peptide.

XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
 KW acute cardiovascular disease; therapy.
 XX Homo sapiens.

XX US6136548-A.

XX 24-OCT-2000.

XX 02-SEP-1999; 99US-0388890.

PR 26-JUL-1996; 96US-0686959.

PR 22-NOV-1994; 94US-0347144.

PR 22-NOV-1995; 95WO-US15007.

PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

XX

DR WPI; 2001-030939/04.
 XX
 PT Identifying mutant tissue-type plasminogen activator (t-PA) for
 PT improving thrombolytic therapy or treating vascular hemorrhaging, by
 PT determining whether t-PA binds to fibrin but not to a beta amyloid
 PT peptide
 XX
 PS Example 3; Column 26; 23pp; English.
 XX
 CC The present invention describes a method for identifying mutant
 CC derivatives of tissue-type plasminogen activator, which involves
 CC determining whether or not they bind to beta-amyloid peptides and fibrin.
 CC Mutants will only bind to the latter. These mutants are useful in
 CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
 CC and in the treatment of acute cardiovascular disease, which may be caused
 CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.
 XX
 SQ Sequence 28 AA;
 Query Match 100.0%; Score 55; DB 22; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00042;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFAQ 10
 Db 13 hhqklvffag 22
 RESULT 4
 AAB91803
 ID AAB91803 standard; Peptide; 35 AA.
 XX
 AC AAB91803;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:979.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 PS Disclosure; Page 514; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 55; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFAQ 10
 Db 8 hhqklvffag 17
 RESULT 5
 AAB91830
 ID AAB91830 standard; Peptide; 35 AA.
 XX
 AC AAB91830;
 XX
 DT 22-JUN-2001 (first entry)
 XX
 DE Amyloid beta-protein fragment peptide SEQ ID NO:1006.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 PS Disclosure; Page 524; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 55; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.00053;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 Db 8 hhqklvffaq 17

RESULT 6

AAW47232
 ID AAW47232 standard; peptide; 40 AA.

XX AC AAW47232;

XX DT 22-MAY-1998 (first entry)

XX DE Beta-amyloid peptide fragment.

XX KW Screening assay; beta-amyloid peptide; treatment;
 amyloidosis disease; Alzheimer's disease.

XX OS Homo sapiens.

XX PN US5721106-A.

XX PD 24-FEB-1998.

XX PF 12-SEP-1994; 94US-0304585.

XX PR 12-SEP-1994; 94US-0304585.

XX PR 13-AUG-1991; 91US-0744767.

XX PA (HARD) HARVARD COLLEGE.

XX PA (MINU) UNIV MINNESOTA.

XX PI Maggio JE, Mantyh PW;

XX WPI; 1998-168404/15.

XX New in vitro screening assay for Alzheimer's disease drugs -
 comprises assessing binding of labelled beta-amyloid peptide to silk
 sample

XX Disclosure; Columns 31-32; 36pp; English.

XX The present sequence was used in the development of a novel in
 CC vitro screening assay for agents capable of affecting the
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method
 CC comprises contacting a silk sample with labelled BAP, optionally
 CC in the presence of a test agent, detecting the amount of label
 CC bound to the silk and assessing the effect of the agent on the
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are
 CC potentially useful for treating amyloidosis diseases, especially
 CC Alzheimer's disease.

XX SQ Sequence 40 AA;

Query Match 100.0%; Score 55; DB 19; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.00062;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFAQ 10
 Db 13 hhqklvffaq 22

RESULT 7

AAW55697
 ID AAR55697 standard; Protein; 53 AA.

XX AC AAR55697;

XX DT 29-DEC-1994 (first entry)

XX DE Sequence of unidentified protein sequence ID number 22.

XX KW Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers;
 transgene; ss.

XX OS Synthetic.

XX PN WO9412627-A.

XX PD 09-JUN-1994.

XX PF 24-NOV-1993; 93WO-US11480.

XX PR 25-NOV-1992; 92US-0989850.

XX PR 09-NOV-1993; 93US-0149222.

XX PA (CEPH-) CEPHALON INC.

XX PI Howland DS, Scott RW;

XX WPI; 1994-200256/24.

XX Transgenic animal model for Alzheimer's disease - contains
 transgene encoding amyloid protein under transcriptional control
 of synapsin gene promoter

XX Example; Page 55; 94pp; English.

XX There was no apparent reference to sequence ID numbers 20, 21 or 22
 in the specification. The specification describes a transgenic
 CC animal model for Alzheimer's disease. A transgenic animal
 CC harbouring a transgene coding for an amyloid protein under the
 CC control of a promoter is claimed. The coding sequence may contain a
 CC APP695, APP751 or APP770. The coding sequence may contain a
 CC mutation, including the hereditary cerebral haemorrhage with
 CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's
 CC disease (FAD). Perhaps SQ IDs 20-22 corresp. to wt, HCHWA-DT
 CC and FAD?

XX SQ Sequence 53 AA;

Query Match 100.0%; Score 55; DB 15; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.00084;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 Db 17 hhqklvffaq 26

RESULT 8

AAW26511
 ID AAW26511 standard; Peptide; 63 AA.

XX AC AAW26511;

XX DT 06-JAN-1998 (first entry)

XX Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).

DE XX

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
 KW substrate; mutin; secretase; Alzheimer's disease;
 KW hereditary cerebral haemorrhage with amyloidosis; human.

OS Homo sapiens.

XX

XX Key Location/Qualifiers
 FT Peptide 10..51
 FT /label= BAP(E22Q)
 FT /note= "beta-amyloid protein E22Q mutant"
 FT Cleavage-site 25..26
 FT /note= "secretase cleavage site"
 FT Domain 38..61
 FT /label= Transmembrane

XX

PN US5656477-A.

XX

XX 12-AUG-1997.

XX

XX 01-MAY-1992; 92US-0877675.

XX

XX 20-SEP-1993; 93US-0123659.

XX

XX 01-MAY-1992; 92US-0877675.

XX

XX (AMCY) AMERICAN CYANAMID CO.

XX

XX Jacobsen JS, Vitek MP;
 WPI; 1997-414594/38.

XX

XX Nucleic acid encoding amyloid precursor mutin(s) - comprising
 PT reporter gene and coding sequence, for identifying compounds which
 PT modify the activity of proteolytic enzymes which cleave APP

XX

PS Disclosure; Fig 5A; 84pp; English.

XX

XX This peptide sequence shows the region of amyloid precursor protein
 CC (APP) that includes a beta-amyloid protein (BAP) carrying a point
 CC mutation (BAP E22Q) found in patients with hereditary cerebral
 CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an
 CC attempt to engineer an APP non-cleavable substrate for secretase,
 CC an APP-reporter (APP-REP) protein that carries the E22Q mutation
 CC has been expressed in recombinant host cells. This resulted in the
 CC secretion of an N-terminal fragment indistinguishable from that of
 CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be
 CC used to detect other putative abnormal APP processing events. They
 CC can also be used to investigate cellular post-translational
 CC modifications to APP in order to determine the potential influence
 CC on normal secretase and abnormal BAP 'clipping' activities.

XX

SQ Sequence 63 AA;

Query Match 100.0%; Score 55; DB 18; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 Db 22 hhqklvffaq 31

RESULT 9
 AAW26391
 ID AAW26391 standard; Peptide; 63 AA.
 XX
 AC AAW26391;
 XX
 DT 15-DEC-1997 (first entry)
 XX

DE XX

XX Amyloid precursor protein fragment APP-REP 751 (BAP E22Q).

KW Amyloid precursor protein; APP; beta-amyloid protein; BAP;
 KW substrate; mutin; secretase; Alzheimer's disease;
 KW hereditary cerebral haemorrhage with amyloidosis; human.

OS Homo sapiens.

XX

XX Key Location/Qualifiers
 FT Peptide 10..51
 FT /label= BAP(E22Q)
 FT /note= "beta-amyloid protein E22Q mutant"
 FT Cleavage-site 25..26
 FT /note= "secretase cleavage site"
 FT Domain 38..61
 FT /label= Transmembrane

XX

PN US5652092-A.

XX

XX 29-JUL-1997.

XX

XX 01-MAY-1992; 92US-0877675.

XX

XX 20-SEP-1993; 93US-0123659.

XX

XX 01-MAY-1992; 92US-0877675.

XX

XX 05-JUN-1995; 95US-0462859.

XX

XX (AMCY) AMERICAN CYANAMID CO.

XX

XX Jacobsen JS, Vitek MP;
 WPI; 1997-392937/36.

XX

XX Screening for compounds which reduce beta-amyloid protein formation
 PT - using cells which express a construct encoding a marker and an
 PT amyloid precursor mutin derived from APP isoforms

XX

PS Disclosure; Fig 5A; 84pp; English.

XX

XX This peptide sequence shows the region of amyloid precursor protein
 CC (APP) that includes a beta-amyloid protein (BAP) carrying a point
 CC mutation (BAP E22Q) found in patients with hereditary cerebral
 CC haemorrhage with amyloidosis of Dutch origin (HCHWA-D). In an
 CC attempt to engineer an APP non-cleavable substrate for secretase,
 CC an APP-reporter (APP-REP) protein that carries the E22Q mutation
 CC has been expressed in recombinant host cells. This resulted in the
 CC secretion of an N-terminal fragment indistinguishable from that of
 CC APP-REP 751 (see AAW26393-94). Non-cleavable APP substrates can be
 CC used to detect other putative abnormal APP processing events. They
 CC can also be used to investigate cellular post-translational
 CC modifications to APP in order to determine the potential influence
 CC on normal secretase and abnormal BAP 'clipping' activities.

XX

SQ Sequence 63 AA;

Query Match 100.0%; Score 55; DB 18; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 Db 22 hhqklvffaq 31

RESULT 10
 AAW44746
 ID AAW44746 standard; Protein; 63 AA.
 XX
 AC AAW44746;
 XX
 DT 01-JUN-1998 (first entry)
 XX

DE APP-REP 751 [BAP E22Q] peptide.
 XX
 KW Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
 KW Alzheimer's disease; cleavage.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 25..26
 FT /note= "secretase cleavage site"
 FT
 FT Misc-difference 31
 FT /note= "Glu to Gln change from wild type sequence"
 FT
 XX
 PN US5693478-A.
 XX
 XX 02-DEC-1997.
 XX
 XX 05-JUN-1995; 95US-0464247.
 XX
 XX 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 PR 05-JUN-1995; 95US-0464247.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Jacobsen JS, Vitek MP;
 XX WPI: 1998-031744/03.
 DR
 XX Amyloid precursor mutin reporter molecule assay containing antibody
 PT recognised marker - used to study pathways associated with
 PT Alzheimer's disease
 XX
 PS Disclosure: Fig 5A; 84pp; English.
 XX
 XX This sequence represent the beta-amyloid protein sequence from the
 CC construct APP-REP751 [BAP E22Q]. The mutant sequence can be used in a
 CC method to study secretase and beta-amyloid protein (BAP)-generating
 CC pathways associated with Alzheimer's disease by studying proteolytic
 CC cleavage of the reporter polypeptides (e.g. AAW44744 and AAW44745).
 XX
 SQ Sequence 63 AA;
 Query Match 100.0%; Score 55; DB 19; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHQKLVFFAQ 10
 Db 22 hhqklvffaq 31
 |||||
 RESULT 11
 AAW42975
 ID AAW42975 standard; peptide; 63 AA.
 XX
 AC AAW42975;
 XX
 XX 01-MAY-1998 (first entry)
 DE
 DE Beta-amyloid peptide (BAP) E22Q.
 KW Beta-amyloid peptide; BAP; extracellular BAP plaque; amyloidosis;
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KW Dutch origin; amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage; hereditary cerebral haemorrhage.
 XX
 OS Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers

FT Domain 38..61
 FT /note= "putative transmembrane domain"
 FT Misc_feature 22
 FT /label= E22Q
 FT /note= "wild type Glu replaced with Gln"
 XX
 PN US5703209-A.
 XX
 XX 30-DEC-1997.
 XX
 XX 05-JUN-1995; 95US-0464248.
 PF
 XX 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Jacobsen JS, Vitek MP;
 XX WPI: 1998-076482/07.
 XX
 XX Amyloid precursor protein fusion polypeptides - comprising APP
 PT fragment and marker, useful for research and drug screening
 PT
 XX
 PS Disclosure: Fig 5A; 84pp; English.
 XX
 XX The present sequence represents a beta-amyloid peptide (BAP) with a
 CC E22Q mutation. Abnormal accumulation of extracellular BAP in plaques
 CC and cerebrovascular deposits is characteristic in brains of individuals
 CC suffering from Alzheimers disease and Downs syndrome. BAP is a poorly
 CC soluble, self-aggregating protein which is derived from a larger amyloid
 CC precursor protein (APP). APP is expressed as an integral membrane
 CC protein, and is cleaved by secretase, between BAP 16Lys and 17Leu.
 CC Cleavage at this site precludes amyloidogenesis and results in the
 CC release of the amino-terminal APP fragment. The E22Q mutation in BAP is
 CC found within the APP of patients with hereditary cerebral haemorrhage
 CC with amyloidosis of Dutch origin, and may be due to an alteration in the
 CC rate of BAP aggregation. APP can be used as a substrate for studying
 CC abnormal proteolytic cleavage which results in the release of BAP, and
 CC also to screen for drugs that will inhibit such cleavage.
 XX
 SQ Sequence 63 AA;
 Query Match 100.0%; Score 55; DB 19; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0.001;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 HHQKLVFFAQ 10
 Db 22 hhqklvffaq 31
 |||||
 RESULT 12
 AAR74695
 ID AAR74695 standard; Peptide; 99 AA.
 XX
 AC AAR74695;
 XX
 XX 11-NOV-1995 (first entry)
 DT
 DE Beta-amyloid precursor protein mutant C-terminal peptide.
 XX
 KW Human; beta-amyloid precursor protein mutant; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX EP653154-A.
 PN
 XX 17-MAY-1995.
 PD
 XX

PF 07-NOV-1994; 94EP-0117512.
 XX
 PR 12-NOV-1993; 93JP-0306026.
 XX
 PA (FARH) HOECHST JAPAN LTD.
 PA (FARH) HOECHST JAPAN KK.
 XX
 XX Kavarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 XX WPI; 1995-180492/24;
 DR N-PSDB; AAQ88697.
 XX
 XX Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 PT over-expression in various cell types
 XX
 XX Claim 2; Page 13; 32pp; English.
 XX
 XX The sequence represents a human brain beta-amyloid precursor protein
 CC (APP) C-terminal peptide. The peptide is a Gln-22 mutant of
 CC AAR74694. DNA encoding the peptide may be transferred, along
 CC with a signal peptide (e.g. AAR74693) gene into somatic and germ
 CC cells of a non-human mammal, and the resulting transgenic animal
 CC may be used as a model for Alzheimer disease (AD). The animal
 CC model exhibits symptoms similar to AD, producing large quantities
 CC of APP C-terminal peptide, death of neuron cells in pyramidal
 CC cells at cerebral amyloid regions, increases in glial cells and
 CC deposition of abnormally phosphorylated tau protein. The animal
 CC model may be used to develop new therapies for AD, including
 CC gene therapy strategies.
 XX
 XX Sequence 99 AA;
 SQ

Query Match 100.0%; Score 55; DB 16; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 Db 13 hhqklvffaq 22
 |||||

RESULT 13
 AAB46225
 ID AAB46225 standard; peptide; 10 AA.
 XX
 AC AAB46225;
 XX
 DT 04-APR-2001 (first entry)
 XX
 XX Human APP derived immunogenic peptide #21.
 XX
 XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 XX Homo sapiens.
 OS
 XX W0200072880-A2.
 PN
 XX 07-DEC-2000.
 PD
 XX
 XX 26-MAY-2000; 2000WO-US14810.
 PF
 XX
 XX 28-MAY-1999; 99US-0322289.
 PR
 XX
 XX (NEUR-) NEURALAB LTD.
 PA
 XX Schenk DB, Bard F, Vasquez NJ, Yednock T;
 PI
 XX WPI; 2001-032104/04.
 DR
 XX

PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody
 XX
 XX Disclosure; Figure 19; 143pp; English.
 XX
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 SQ Sequence 10 AA;
 SQ

Query Match 94.5%; Score 52; DB 22; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.00054;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 Db 1 hhqklvffae 10
 |||||

RESULT 14
 AAW89358
 ID AAW89358 standard; peptide; 15 AA.
 XX
 AC AAW89358;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 XX Beta-amyloid peptide derivative A-beta-11-25.
 XX
 XX Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
 KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
 KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
 KW Creutzfeldt-Jakob disease; BAP.
 XX
 XX Homo sapiens.
 OS
 XX Synthetic.
 XX
 XX US5854204-A.
 PN
 XX 29-DEC-1998.
 PD
 XX
 XX 14-MAR-1996; 96US-0612785.
 PF
 XX
 XX 14-MAR-1996; 96US-0612785.
 PR
 XX 14-MAR-1995; 95US-0404831.
 PR
 XX 07-JUN-1995; 95US-0475579.
 PR
 XX 27-OCT-1995; 95US-0548998.
 PR
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 PA
 XX Benjamin H, Chin J, Findeis MA, Garnick MB, Geffer ML;
 PI Hundal A, Kasman L, Kelley M, Kubasek W, Lee J;
 PI Molineaux S, Musso G, Reed M, Signer ER, Wakefield J;
 XX
 XX WPI; 1999-094964/08.
 DR
 XX New peptide(s) derived from beta-amyloid peptide that inhibit
 PT amyloid aggregation - and neurotoxicity, specifically for treatment
 PT and prevention of Alzheimer's disease
 XX

PS Claim 6; Column 81-82; 52pp; English.

XX The present invention describes beta-amyloid peptide (bAP) derivatives.
 CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
 CC peptides, specifically bAP, and their neurotoxicity, so are useful for
 CC treating and preventing any disease involving amyloidosis, specifically
 CC Alzheimer's disease but also Down's syndrome, familial amyloid
 CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
 CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
 CC these diseases, in vitro or in vivo, by detecting binding of bAP to
 CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
 CC even when bAP is present in molar excess. The present sequence
 CC represents a bAP derivative.
 XX
 SQ Sequence 15 AA;

Query Match 94.5%; Score 52; DB 20; Length 15;

Best Local Similarity 90.0%; Pred. No. 0.00084;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 DB 3 hhgklvfae 12

RESULT 15

AAR54703
 ID AAR54703 standard; peptide; 17 AA.

XX AAR54703;

XX DT 15-DEC-1994 (first entry)

XX DE Beta-amyloid fragment (12-28).

XX KW Beta-amyloid protein; BAP; Alzheimer's disease; diagnosis.

XX OS Homo sapiens.

XX PN W09409364-A.

XX PD 28-APR-1994.

XX PF 13-OCT-1993; 93WO-US09772.

XX PR 13-OCT-1992; 92US-0959251.

XX PA (UYDU-) UNIV DUKE.

XX PI Strittmatter WJ;

XX DR WPI; 1994-151484/18.

XX PT Immobilised beta-amyloid protein or fragments - used in assays
 for obtaining prods for use in the diagnosis and treatment of
 disorders such as Alzheimer's disease.

PS Claim 5; Page 28; 49pp; English.

XX A construct comprising a beta-amyloid protein (BAP) or fragment (esp.
 CC the peptides given in AAR54702-03) immobilised on a solid support can be
 CC used to detect cpds which bind to BAP. Binding of proteins in
 CC human cerebrospinal fluid proteins were shown to bind to beta-
 CC amyloid peptides 1-28 and 12-28. Hydropathic mimic peptide (12-28)
 CC was used as control.
 XX

SQ Sequence 17 AA;

Query Match

Best Local Similarity 94.5%; Score 52; DB 15; Length 17;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 DB 2 hhgklvfae 11

Search completed: July 18, 2002, 10:16:10
 Job time: 197 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:14:38 ; Search time 14.76 Seconds
(without alignments)
65.101 Million cell updates/sec

Title: US-09-724-842-27

Perfect score: 55

Sequence: 1 HHQKLVFFAQ 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 71:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	94.5	42	2 PN0512	beta-amyloid prote
2	52	94.5	57	2 E60045	Alzheimer's diseas
3	52	94.5	57	2 F60045	Alzheimer's diseas
4	52	94.5	57	2 G60045	Alzheimer's diseas
5	52	94.5	57	2 D60045	Alzheimer's diseas
6	52	94.5	57	2 A60045	Alzheimer's diseas
7	52	94.5	57	2 B60045	Alzheimer's diseas
8	52	94.5	82	2 PQ0438	Alzheimer's diseas
9	52	94.5	695	1 A49795	Alzheimer's diseas
10	52	94.5	747	2 JH0773	Alzheimer's diseas
11	52	94.5	770	1 QH0044	Alzheimer's diseas
12	44	80.0	33	2 S23094	Alzheimer's diseas
13	44	80.0	695	2 A27485	beta-amyloid prote
14	44	80.0	695	2 S00550	Alzheimer's diseas
15	41	74.5	549	1 N00C	Alzheimer's diseas
16	41	74.5	549	2 H91254	glucose-6-phosphat
17	41	74.5	549	2 D86095	glucosephosphate 1
18	41	74.5	549	2 AD1013	glucosephosphate 1
19	41	74.5	550	2 B82330	glucose-6-phosphat
20	40	72.7	191	2 T04853	glucose-6-phosphat
21	39	70.9	699	2 H64118	hypothetical prote
22	38	69.1	272	2 F70979	4-alpha-glucanotra
23	38	69.1	549	2 G84996	hypothetical prote
24	37	67.3	635	2 H81793	glucose-6-phosphat
25	36	65.5	210	2 I58391	hypothetical prote
26	36	65.5	563	2 F64130	sarcoma amplified
27	36	65.5	859	2 F69159	glucose-6-phosphat
28	36	65.5	1668	1 C69224	protoporphyrin IX
29	35	63.6	297	2 T23909	cobalamin biosynth
					hypothetical prote

30 35 63.6 446 2 T50786
31 35 63.6 548 2 AF0452
32 35 63.6 552 2 T25496
33 35 63.6 850 2 JC5047
34 34 61.8 140 2 C81176
35 34 61.8 590 2 F95853
36 34 61.8 763 2 S51300
37 34 61.8 1035 2 T42093
38 34 61.8 1036 2 T13732
39 34 61.8 1036 2 T18530
40 34 61.8 1037 2 T13943
41 34 61.8 1074 2 T17203
42 34 61.8 1074 2 T13725
43 34 61.8 1075 2 T46635
44 34 61.8 1163 2 S07137
45 34 61.8 1375 2 T18961

ALIGNMENTS

RESULT 1

beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C:Accession: PN0512

R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohn

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fr

A:Reference number: PN0512; MUID:93290653

A:Accession: PN0512

A:Molecule type: protein

A:Residues: 1-42 <SH1>

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteina

C:Keywords: alternative splicing; amyloid

Query Match 94.5%; Score 52; DB 2; Length 42;

Best Local Similarity 90.0%; Pred. No. 0.0011;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10

DB 13 HHQKLVFFAE 22

|||||||

RESULT 2

E60045

Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)

C:Species: Ovis sp. (sheep)

C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: E60045

R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991

A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in

A:Reference number: A60045; MUID:92017079

A:Accession: E60045

A:Molecule type: mRNA

A:Residues: 1-57 <JOH>

A:Cross-references: EMBL:X56130

C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteina

C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match

Best Local Similarity 94.5%; Score 52; DB 2; Length 57;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10

DB 18 HHQKLVFFAE 27

|||||||

RESULT 3
 F60045
 Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: F60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog.
 A:Reference number: A60045; MUID:92017079
 A:Accession: F60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:g1896
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;
 Best Local Similarity 90.0%; Pred. No. 0.0015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 DB 18 HHQKLVFFAE 27

RESULT 4
 G60045
 Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: G60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog.
 A:Reference number: A60045; MUID:92017079
 A:Accession: G60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56126
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;
 Best Local Similarity 90.0%; Pred. No. 0.0015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 DB 18 HHQKLVFFAE 27

RESULT 5
 D60045
 Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: D60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog.
 A:Reference number: A60045; MUID:92017079
 A:Accession: D60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56124
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;
 Best Local Similarity 90.0%; Pred. No. 0.0015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 DB 18 HHQKLVFFAE 27

Query Match 94.5%; Score 52; DB 2; Length 57;
 Best Local Similarity 90.0%; Pred. No. 0.0015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 DB 18 HHQKLVFFAE 27

RESULT 6
 A60045
 Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
 C:Accession: A60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 A:Accession: A60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56125
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;
 Best Local Similarity 90.0%; Pred. No. 0.0015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 DB 18 HHQKLVFFAE 27

RESULT 7
 B60045
 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C:Species: Ursus maritimus (polar bear)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: B60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
 A:Reference number: A60045; MUID:92017079
 A:Accession: B60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 94.5%; Score 52; DB 2; Length 57;
 Best Local Similarity 90.0%; Pred. No. 0.0015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 DB 18 HHQKLVFFAE 27

RESULT 8
 P00438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C:Accession: P00438; C60045
 R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
 A:Reference number: P00438; MUID:93075180

A:Accession: PQ0438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>
 A:Cross-references: GB:M83558; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog.
 A:Reference number: A60045; MUID:92017079
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 94.5%; Score 52; DB 2; Length 82;
 Best Local Similarity 90.0%; Pred. No. 0.0022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFAQ 10
 |||||
 DB 29 HHQKLVFFAE 38

RESULT 9

A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 A:Accession: A49795
 R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a P
 A:Reference number: A49795; MUID:91273117
 A:Accession: A49795
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-695 <POD>
 A:Cross-references: GB:M58727; NID:G342062; PIDN:AAA36829.1; PID:G342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing

Query Match 94.5%; Score 52; DB 1; Length 695;
 Best Local Similarity 90.0%; Pred. No. 0.021;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFAQ 10
 |||||
 DB 609 HHQKLVFFAE 618

RESULT 10

JH0773
 Alzheimer's disease amyloid beta protein precursor - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
 A:Accession: JH0773
 R:Okado, H.; Okamoto, H.
 Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
 A:Title: A xenopus homologue of the human beta-amyloid precursor protein: developmental
 A:Reference number: JH0773; MUID:93129227
 A:Accession: JH0773
 A:Molecule type: mRNA
 A:Residues: 1-747 <OKA>
 A:Cross-references: GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:G263151
 A:Experimental source: larva
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1
 C:Keywords: alternative splicing; amyloid
 F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 94.5%; Score 52; DB 2; Length 747;
 Best Local Similarity 90.0%; Pred. No. 0.023;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFAQ 10
 |||||
 DB 661 HHQKLVFFAE 670

RESULT 11

QRHUM4
 Alzheimer's disease amyloid beta protein precursor [validated] - human
 N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor XIA II
 C:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vasc
 protein precursor splice form APP(770)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
 A:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562;
 4668; A28583; A29302; A0805; JLO038; S06121; A60355; A59011; A38384; S29076; S38522
 R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;
 Nucleic Acids Res. 17, 517-522, 1989
 A:Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded
 A:Reference number: S02260; MUID:89128427
 A:Accession: S02260
 A:Molecule type: DNA
 A:Residues: 1-288, 'V', 365-770 <LEMI>
 A:Cross-references: EMBL:X13466
 A:Note: alternative splice form APP(695)
 R:Lemaire, H.G.
 submitted to the EMBL Data Library, November 1988
 A:Reference number: S05194
 A:Accession: S05194
 A:Molecule type: DNA
 A:Residues: 1-14, 'VW', 17-288, 'V', 365-770 <LEM2>
 A:Cross-references: EMBL:X13466; NID:G35598; PIDN:CAA31830.1; PID:G871360
 A:Note: alternative splice form APP(695)
 R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
 Biochem. Biophys. Res. Commun. 159, 297-304, 1989
 A:Title: Characterization of the 5'-end region and the first two exons of the beta-p
 A:Reference number: A32277; MUID:89165870
 A:Accession: A32277
 A:Molecule type: DNA
 A:Residues: 1-75 <LAF>
 A:Cross-references: GB:M24546; GB:M24547; NID:G341202; PIDN:AAC13654.1; PID:G516074
 R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.;
 Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
 A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simil
 A:Reference number: A33260; MUID:89392030
 A:Accession: A33260
 A:Molecule type: DNA
 A:Residues: 656-737 <JOH>
 A:Cross-references: GB:M29270; NID:G178863; PIDN:AAA51768.1; PID:G178865
 R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione,
 Biochem. Biophys. Res. Commun. 170, 301-307, 1990
 A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
 A:Reference number: A35486; MUID:90321244
 A:Accession: A35486
 A:Molecule type: DNA
 A:Residues: 672-710 <PREI>
 A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
 R:Yoshikawa, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 87, 257-263, 1990
 A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
 A:Reference number: I39451; MUID:90236318
 A:Accession: I39452
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB
 A:Molecule type: DNA
 A:Residues: 1-770 <YOSI>
 A:Cross-references: GB:X33112; NID:G178613; PIDN:AAB59502.1; PID:G178616
 A:Accession: I39451
 A:Status: nucleic acid sequence not shown; translation not shown; translated from GB
 A:Molecule type: DNA
 A:Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>

A:Cross-references: GB:M34875; NID:g178608; PIDN:AA59501.1; PID:g178615
 R:Foshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
 Gene 102, 291-292, 1991
 A:Reference number: A59020; MUID:91340168
 A:Contents: annotation; erratum
 A:Note: revised physical map for reference I39451
 R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
 Science 248, 1124-1126, 1990
 A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrhage
 A:Reference number: I39453; MUID:90260663
 A:Accession: I39453
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 656-737 <LEV>
 A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
 A:Note: a mutation with 693-Gln is presented
 R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
 Science 254, 97-99, 1991
 A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer's disease
 A:Reference number: I59562; MUID:92022553
 A:Accession: I59562
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 689-716, 'E', 718-737 <WR>
 A:Cross-references: GB:S57665; NID:g236720; PIDN:AA19991.1; PID:g236721
 R:Kamino, K.; Ori, H.T.; Payami, H.; Wijman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
 arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
 Am. J. Hum. Genet. 51, 998-1014, 1992
 A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
 A:Reference number: A44017; MUID:93035397
 A:Accession: A44017
 A:Molecule type: DNA
 A:Residues: 687-692, 'G', 694-718 <RAM1>
 A:Cross-references: GB:S45135; NID:g257377; PIDN:AA23645.1; PID:g257378
 A:Experimental source: familial Alzheimer disease family SB
 A:Note: sequence extracted from NCBI database (NCBIP:115374)
 A:Accession: B44017
 A:Molecule type: DNA
 A:Residues: 687-718 <RAM2>
 A:Cross-references: GB:S45136; NID:g257379; PIDN:AA23646.1; PID:g257380
 A:Experimental source: familial Alzheimer disease family LIT
 A:Note: sequence extracted from NCBI database (NCBIP:115376)
 A:Note: this sequence has a silent mutation
 R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
 Nature 325, 733-736, 1987
 A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
 A:Reference number: A03134; MUID:87144572
 A:Accession: A03134
 A:Molecule type: mRNA
 A:Residues: 1-288, 'V', 365-770 <KAN>
 A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
 A:Note: alternative splice form APP(695)
 R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
 A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
 A:Reference number: A29030; MUID:87231971
 A:Accession: A29030
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
 A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
 A:Note: the authors translated the codon GAG for residue 647 as Asp
 R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
 Science 235, 877-880, 1987
 A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
 A:Reference number: A47584; MUID:87120328
 A:Accession: A47584
 A:Molecule type: mRNA
 A:Residues: 674-756, 'S', 758-770 <GOL>
 A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
 A:Experimental source: brain
 R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
 Science 235, 880-884, 1987
 A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th

A:Reference number: A47585; MUID:87120329
 A:Accession: A47585
 A:Molecule type: mRNA
 A:Residues: 674-703 <TANI>
 A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
 R:Dykes, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
 EMBO J. 7, 949-957, 1988
 A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4
 A:Reference number: S02638; MUID:88296437
 A:Accession: S02638
 A:Molecule type: mRNA
 A:Residues: 672-678 <DYR>
 R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; P
 Nature 331, 528-530, 1988
 A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA asso
 A:Reference number: S00707; MUID:88122640
 A:Accession: S00707
 A:Molecule type: mRNA
 A:Residues: 286-344, 'I', 365-366 <TAN2>
 A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
 A:Experimental source: promyelocytic leukemia cell line HL60
 A:Note: alternative splice form APP(751)
 R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
 Nature 331, 525-527, 1988
 A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
 A:Reference number: S00925; MUID:88122639
 A:Accession: S00925
 A:Molecule type: mRNA
 A:Residues: 1-344, 'I', 365-770 <PO2>
 A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
 A:Note: alternative splice form APP(751)
 R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
 Nature 331, 530-532, 1988
 A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
 A:Reference number: A38949; MUID:88122641
 A:Accession: A38949
 A:Molecule type: mRNA
 A:Residues: 287-367 <KIT>
 A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
 A:Experimental source: glioblastoma cell line
 A:Note: alternative splice form APP(770)
 R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
 Brain Res. Mol. Brain Res. 4, 121-131, 1988
 A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
 A:Reference number: A30320
 A:Accession: A30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 284-288, 'V', 365-770 <VIT1>
 A:Accession: B30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 122-288, 'V', 365-770 <VIT2>
 A:Accession: C30320
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 606-770 <VIT3>
 R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
 Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
 A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
 A:Reference number: A31087; MUID:88124954
 A:Accession: A31087
 A:Molecule type: mRNA
 A:Residues: 507-770 <ZAI>
 A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
 A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
 8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
 A:Note: the cited Genbank accession number, J03594, is not in release 101.0
 R:Masters, C.L.; Multhaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther,
 Query Match 94.5%; Score 52; DB 1; Length 770;
 Best Local Similarity 90.0%; Pred. No. 0.023; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0

QY 1 HHOKLVFFAQ 10
|||||||:
Db 684 HHOKLVFFAE 693

RESULT 12

S23094
beta-amyloid protein precursor - rat
N:Alternate names: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C:Accession: S23094
R:Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A:Reference number: S23094; MUID:92316198
A:Accession: S23094
A:Molecule type: protein
A:Residues: 1-33 <KOJ>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 80.0%; Score 44; DB 2; Length 33;
Best Local Similarity 88.9%; Pred. No. 0.035;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHOKLVFFAQ 10
|||||||:
Db 19 HHOKLVFFAE 27

RESULT 13

A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N:Alternate names: proteinase nexin II
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
C:Accession: A27485; S19727; I49485
R:Yamada, T.; Sakaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
A:Reference number: A27485; MUID:88106489
A:Accession: A27485
A:Molecule type: mRNA
A:Residues: 1-695 <YAM>
A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g303085
A:Experimental source: brain
R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A:Reference number: S19727; MUID:92096458
A:Accession: S19727
A:Molecule type: mRNA
A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A:Cross-references: EMBL:X59379
R:Izumii, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
A:Reference number: I49485; MUID:92209998
A:Accession: I49485
A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-19 <RES>
A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
C:Genetics:
A:Map position: 16C3
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 80.0%; Score 44; DB 2; Length 695;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHOKLVFFAQ 10
|||||||:
Db 610 HHOKLVFFAE 618

RESULT 14

S00550
Alzheimer's disease amyloid beta protein precursor - rat
N:Alternate names: beta-A4 amyloid protein
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
C:Accession: S00550; A41245; A39820; S46251
R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.
EMBO J. 7, 1365-1370, 1988
A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat
A:Reference number: S00550; MUID:88312583
A:Accession: S00550
A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan
A:Reference number: A41245; MUID:88264430
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat
A:Reference number: A39820; MUID:91217087
A:Accession: A39820
A>Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/Domain: transmembrane #status predicted <TM>

Query Match 80.0%; Score 44; DB 2; Length 695;
Best Local Similarity 88.9%; Pred. No. 0.84;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHOKLVFFAQ 10
|||||||:
Db 610 HHOKLVFFAE 618

RESULT 15

NUEC
glucose-6-phosphate isomerase (EC 5.3.1.9) - Escherichia coli
N:Alternate names: phosphoglucose isomerase; phosphohexose isomerase
C:Species: Escherichia coli
C:Date: 31-Mar-1990 #sequence_revision 17-Oct-1997 #text_change 08-Sep-2000
C:Accession: H65209; JS0142; S04396
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H65209
A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-549 <BLAT>
 A:Cross-references: GB:AE000476; GB:U00096; NID:gl790456; PIDN:AAC76995.1; PID:gl790457;
 A:Experimental source: strain K-12, substrain MG1655
 R:Froman, B.E.; Tait, R.C.; Gottlieb, L.D.
 Mol. Gen. Genet. 217, 126-131, 1989
 A:Title: Isolation and characterization of the phosphoglucose isomerase gene from Escher
 A:Reference number: JS0142; MUID:89364675
 A:Accession: JS0142
 A:Molecule type: DNA
 A:Residues: 1-316,'V',318-549 <PRO>
 A:Cross-references: GB:X15196; NID:g42376; PIDN:CAA33268.1; PID:g42377
 A:Experimental source: strain JMI01
 A:Note: the authors translated the codon CAG for residue 8 as Trp
 C:Comment: This enzyme catalyzes the reversible isomerization of glucose-6-phosphate and
 C:Genetics:
 A:Gene: pgi
 A:Map position: 91 min
 A:Superfamily: glucose-6-phosphate isomerase
 C:Keywords: glycolysis; homodimer; intramolecular oxidoreductase; isomerase
 F:514/Active site: Lys #status predicted

Query Match 74.5%; Score 41; DB 1; Length 549;
 Best Local Similarity 75.0%; Pred. No. 2.6;
 Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 HHOKLV--FFAQ 10
 |||||: ||||
 Db 416 HHQKLLSNEFAQ 427

Search completed: July 18, 2002, 10:16:51
 Job time: 133 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:33 ; Search time 10.34 Seconds
(without alignments)
37.446 Million cell updates/sec

Title: US-09-724-842-27
Perfect score: 55
Sequence: 1 HHOKLVFFAQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	94.5	57	A4_PIG	Q29023 sus scrofa
2	52	94.5	57	A4_URSMA	Q29149 ursus marit
3	52	94.5	58	A4_CANFA	Q28280 canis famil
4	52	94.5	58	A4_RABIT	Q28748 ovis aries
5	52	94.5	58	A4_SHEEP	Q28757 ovis aries
6	52	94.5	59	A4_BOVIN	Q28053 bos taurus
7	52	94.5	751	A4_SAISC	Q95241 salmistr sci
8	52	94.5	770	A4_HUMAN	P05067 homo sapien
9	44	80.0	770	A4_MOUSE	P12023 mus musculu
10	44	80.0	770	A4_RAT	P08592 rattus norv
11	41	74.5	549	G6PI_ECOLI	P11537 escherichia
12	41	74.5	550	G6PI_VIBCH	Q9kuy4 vibrio chol
13	39	70.9	699	MALQ_HAEIN	P45176 haemophilus
14	38	69.1	549	G6PI_BUCAL	P57636 buchnera ap
15	38	69.1	549	G6PI_PASMU	Q9cn12 pasteurella
16	36	65.5	109	SAS_PIG	Q29257 sus scrofa
17	36	65.5	204	TNE6_HUMAN	Q95857 homo sapien
18	36	65.5	210	SAS_HUMAN	Q12999 homo sapien
19	36	65.5	549	G6PI_HAEIN	P44312 haemophilus
20	35	63.6	167	G6PI_KLBOX	P77877 klebsiella
21	35	63.6	849	RS62_HUMAN	Q15283 homo sapien
22	34	61.8	763	YNS1_YEAST	P42843 saccharomyc
23	34	61.8	1036	PLD1_CRIGR	Q08684 cricetus
24	34	61.8	1074	PLD1_HUMAN	Q13393 homo sapien
25	34	61.8	1074	PLD1_MOUSE	Q92280 mus musculu
26	34	61.8	1074	PLD1_RAT	P70496 rattus norv
27	34	61.8	1163	RPOD_PEA	P12227 pisum sativ
28	34	61.8	4427	PKSL_BACSU	Q05470 bacillus su
29	33	60.0	214	ACUB_BACSU	P39066 bacillus su
30	33	60.0	278	IOD3_HUMAN	P55073 homo sapien
31	33	60.0	278	IOD3_RAT	P49897 rattus norv
32	33	60.0	325	I10S_HUMAN	Q08334 homo sapien
33	33	60.0	346	ILVC_BUCUE	Q9aq97 buchnera ap

34	33	60.0	421	1	HUT1_BACSU	P42084 bacillus su
35	33	60.0	482	1	PO24_POPJA	Q03275 popillia ja
36	33	60.0	496	1	C7D9_SOYBN	O81971 glycine max
37	33	60.0	564	1	SYT_MYCGE	P47615 mycoplasma
38	33	60.0	754	1	CHLD_PEA	O22437 pisum sativ
39	33	60.0	758	1	CHLD_TOBAC	O24133 nicotiana t
40	33	60.0	759	1	CHLD_ARATH	O9sje1 arabidopsis
41	32	58.2	124	1	SLP_BACSU	P39190 bacillus su
42	32	58.2	321	1	CYF_GUTH	O78494 guillardia
43	32	58.2	332	1	RPSB_ANASP	Q03065 anabaena sp
44	32	58.2	380	1	FD3E_SOYBN	P48625 glycine max
45	32	58.2	462	1	MPPB_YEAST	P10507 saccharomyc

ALIGNMENTS

RESULT	1					
A4_PIG						
ID	A4_PIG	STANDARD;	PRT;	57 AA.		
AC	Q29023:					
DT	01-NOV-1997 (Rel. 35, Created)					
DT	01-NOV-1997 (Rel. 35, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).					
DE	GN APP.					
OS	Sus scrofa (Pig).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.					
OX	NCBI_TaxID=9823;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Brain;					
RA	MEDLINE=92017079; PubMed=1656157;					
RT	Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;					
RT	"Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."					
RL	Brain Res. Mol. Brain Res. 10:299-305(1991).					
CC	FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).					
CC	SUBCELLULAR LOCATION: Type I membrane protein.					
CC	SIMILARITY: BELONGS TO THE APP FAMILY.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC	EMBL; X56127; CAA39592.1;					
DR	HSSP; P05067; 1BA4.					
DR	InterPro; IPR001868; A4_APP.					
DR	PROSITE; PS00319; A4_EXTRA; PARTIAL.					
DR	PROSITE; PS00320; A4_INTRA; PARTIAL.					
KW	Glycoprotein; Amyloid; Neurone; Transmembrane.					
FT	CHAIN 1 1					
FT	DOMAIN <1 33					
FT	TRANSMEM 34 57					
FT	NON_TER 57					
SQ	SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;					

Query Match 94.5% Score 52; DB 1; Length 57;
Best Local Similarity 90.0%; Pred. NO. 0.00081;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Oy 1 HHOKLVFFAQ 10

```

DB 18 HHQKLVFFAE 27
|||||
RESULT 2
A4_URSM 2
ID A4_URSM 2 STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSP; P05067; IAML.
CC InterPro: IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57 POTENTIAL.
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 94.5%; Score 52; DB 1; Length 57;
Best Local Similarity 90.0%; Pred. No. 0.00081;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 18 HHQKLVFFAE 27
|||||
RESULT 3
A4_CANFA 3
ID A4_CANFA 3 STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSP; P05067; IAML.
CC InterPro: IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57 POTENTIAL.
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 94.5%; Score 52; DB 1; Length 58;
Best Local Similarity 90.0%; Pred. No. 0.00082;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 19 HHQKLVFFAE 28
|||||
RESULT 4
A4_RABIT 4
ID A4_RABIT 4 STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -|- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56125; CAA39590.1; -
CC HSP; P05067; IBA4.
CC InterPro: IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutone; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 34 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 35 58 EXTRACELLULAR (POTENTIAL).
FT NON_TER 58 58 POTENTIAL.
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;

Query Match 94.5%; Score 52; DB 1; Length 58;
Best Local Similarity 90.0%; Pred. No. 0.00082;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 19 HHQKLVFFAE 28
|||||

```

RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X56129; CAA39594.1; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001868; A4_APP.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

 Query Match 94.5%; Score 52; DB 1; Length 58;
 Best Local Similarity 90.0%; Pred. No. 0.00082;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFFAQ 10
 DB 18 HHOKLVFFAE 27
 |||||
 RESULT 5
 A4_SHEEP
 ID A4_SHEEP STANDARD; PRT; 58 AA.
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X56130; CAA39595.1; -.
 DR HSSP; P05067; IAML.
 DR InterPro; IPR001868; A4_APP.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 94.5%; Score 52; DB 1; Length 58;
 Best Local Similarity 90.0%; Pred. No. 0.00082;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFFAQ 10
 DB 18 HHOKLVFFAE 27
 |||||
 RESULT 6

A4_BOVIN
 ID A4_BOVIN STANDARD; PRT; 59 AA.
 AC Q28053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -----

This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 DR EMBL; X56124; CAA39589.1; -.
 DR EMBL; X56126; CAA39591.1; -.
 DR HSSP; P05067; IBA4.
 DR InterPro; IPR001868; A4_APP.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane.

SEQUENCE FROM N.A.
MEDLINE=97363807; PubMed=9108164;
Hattori M., Tsukahara F., Furubata Y., Tanahashi H., Hirose M.

RA Saito M., Tsukuni S., Sakaki Y.;
 RT "A novel method for making nested deletions and its application for
 RL sequencing of a 300 kb region of human APP locus.";
 RN Nucleic Acids Res. 25:1802-1808(1997).
 [5]
 RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
 RX MEDLINE=88122640; PubMed=2893290;
 RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
 RA Gusella J.F., Neve R.L.;
 RT "Protease inhibitor domain encoded by an amyloid protein precursor
 RL mRNA associated with Alzheimer's disease.";
 RN Nature 331:528-530(1988).
 [6]
 RP SEQUENCE OF 287-367 FROM N.A.
 RX MEDLINE=88122641; PubMed=2893291;
 RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
 RT "Novel precursor of Alzheimer's disease amyloid protein shows
 RL protease inhibitory activity.";
 RN Nature 331:530-532(1988).
 [7]
 RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
 RX MEDLINE=87231971; PubMed=3035574;
 RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
 RT "Molecular cloning and characterization of a cDNA encoding the
 RL cerebrovascular and the neuritic plaque amyloid peptides.";
 RN Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
 [8]
 RP SEQUENCE OF 507-770 FROM N.A.
 RX MEDLINE=88124954; PubMed=2893379;
 RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
 RA Marotta C.A.;
 RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
 RL disease brain: coding and noncoding regions of the fetal precursor
 RN mRNA are expressed in the cortex.";
 RN Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
 [9]
 RP SEQUENCE OF 672-681.
 RX MEDLINE=88035004; PubMed=3312495;
 RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
 RA Tourtellotte W.W., Huebner V., Shively J.E.;
 RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
 RL and partial sequence of a 4,200-dalton peptide isolated from cortical
 RN microvessels.";
 RN J. Neurochem. 49:1394-1401(1987).
 [10]
 RP SEQUENCE OF 739-770 FROM N.A.
 RX MEDLINE=90236318; PubMed=2110105;
 RA Yoshikawa S.-I., Sakaki H., Doh-Ura K., Furuya H., Sakaki Y.;
 RT "Genomic organization of the human amyloid beta-protein precursor
 RL gene.";
 RN Gene 87:257-263(1990).
 [11]
 RP SEQUENCE OF 1-10 FROM N.A.
 RX MEDLINE=89016647; PubMed=3140222;
 RA Schon E.A., Mita S., Sadlock J., Herbert J.;
 RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
 RL encodes a 95-kDa polypeptide.";
 RN Nucleic Acids Res. 16:9351-9351(1988).
 [12]
 RP SEQUENCE OF 18-50.
 RX MEDLINE=87250462; PubMed=3597385;
 RA van Nostrand W.E., Cunningham D.D.;
 RT "Purification of protease nexin II from human fibroblasts.";
 RN J. Biol. Chem. 262:8508-8514(1987).
 [13]
 RP IDENTIFY OF APP WITH NEXIN-II.
 RX MEDLINE=89384866; PubMed=2506449;
 RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
 RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
 RA Sinha S.;
 RT "The secreted form of the Alzheimer's amyloid precursor protein with
 RL the Kunitz domain is protease nexin-II.";

RL Nature 341:144-147(1989).
 [14]
 RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
 RX MEDLINE=90211252; PubMed=1969731;
 RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
 RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
 RL disease amyloid protein precursor.";
 RN Biochem. Biophys. Res. Commun. 167:716-721(1990).
 [15]
 RP COMPLEX WITH G(O).
 RX MEDLINE=93188965; PubMed=8446172;
 RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
 RA Murayama Y., Ogata E.;
 RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
 RL protein G(O).";
 RN Nature 362:75-79(1993).
 [16]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
 RX MEDLINE=99215582; PubMed=10201399;
 RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
 RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
 RA Parker M.W.;
 RT "Crystal structure of the N-terminal, growth factor-like domain of
 RL Alzheimer amyloid precursor protein.";
 RN Nat. Struct. Biol. 6:327-331(1999).
 [17]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
 RX MEDLINE=91104913; PubMed=2125487;
 RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kosiakof A.A.;
 RT "X-ray crystal structure of the protease inhibitor domain of
 RL Alzheimer's amyloid beta-protein precursor.";
 RN Biochemistry 29:10018-10022(1990).
 [18]
 RP STRUCTURE BY NMR OF 289-344.
 RX MEDLINE=92031488; PubMed=1718421;
 RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayne R.M.,
 RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
 RA Tamburini P.P.;
 RT "Sequential NMR resonance assignment and structure determination of
 RL the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
 RN precursor protein.";
 RN Biochemistry 30:10467-10478(1991).
 [19]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=94281210; PubMed=7516706;
 RA Tafafous J., Marchowski K.J., Klopman G., Zagorski M.G.;
 RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
 RN Biochemistry 33:7788-7796(1994).
 [20]
 RP STRUCTURE BY NMR OF 696-706.
 RX MEDLINE=97128622; PubMed=8973180;
 RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
 RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
 RL membrane-mimicking environment.";
 RN Biochemistry 35:16094-16104(1996).
 [21]
 RP STRUCTURE BY NMR OF 672-711.
 RX MEDLINE=98359783; PubMed=9693002;
 RA Coles M., Bicknell W., Watson A.A., Craik D.J.;
 RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
 RL environment. Is the membrane-spanning domain where we think it is?";
 RN Biochemistry 37:11064-11077(1998).
 [22]
 RP STRUCTURE BY NMR OF 672-699.
 RX MEDLINE=20400066; PubMed=10940222;
 RA Poulsen S.-A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RL peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RN site.";
 RN J. Struct. Biol. 130:142-152(2000).
 [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;

RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RA "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 RN [24]
 RP QUERY MATCH 94.5%; Score 52; DB 1; Length 770;
 RP Best Local Similarity 90.0%; Pred. No. 0.011;
 RP Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFAQ 10
 DB 684 HHQKLVFFAE 693
 RESULT 9
 A4_MOUSE
 ID A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN=BALE/C; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or protease nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88106489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=9209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X59379; ; NOT_ANNOTATED_CDS.
 DR EMBL: M18373; AAA37139.1; -
 DR EMBL: X15210; CAA33280.1; -
 DR EMBL: D10603; BAA01456.1; -
 DR EMBL: M24397; AAA39929.1; -
 DR PIR: A27485; A27485.
 DR PIR: S04853; S04853.
 DR PIR: S19727; S19727.
 DR HSP: P05067; LOCW.
 DR MGD: MGI:88059; App.
 DR InterPro: IPR001868; A4_APP.
 DR InterPro: IPR002223; Kunitz_BPTI.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR Pfam: PF00014; Kunitz_BPTI; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR PRINTS: PR00759; BASICPTASE.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR SMART: SM00131; KU; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neutone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT DOMAIN 18 699
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT VARSPPLIC 289 289
 FT VARSPPLIC 290 364
 FT VARSPPLIC 346 380
 FT SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAF7A CRC64;

Query Match 80.0%; Score 44; DB 1; Length 770;
 Best Local Similarity 88.9%; Pred. No. 0.43;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQKLVFFAQ 10
 DB 685 HQKLVFFAE 693

RESULT 10
 A4_RAT STANDARD; PRT; 770 AA.

AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (Ag).
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 SEQUENCE OF 1-289 AND 365-770 FROM N.A.

RP TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 SEQUENCE OF 289-364 FROM N.A.

RP TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -1- SURCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; X07648; CAA30488.1; -
 DR EMBL; X14066; CAA32229.1; -
 DR PIR; S00550; S00550.
 DR PIR; S03607; S03607.
 DR HSSP; P05067; 1AAP.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR SMART; SM00006; A4_EXTRA; 1.

DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT FT FT
 FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723
 FT DOMAIN 724 770
 FT DOMAIN 673 715
 FT DOMAIN 287 345
 FT SITE 759 762
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 542 542
 FT CARBOHYD 571 571
 FT VARSPPLIC 289 289
 FT VARSPPLIC 290 364
 SQ SEQUENCE 770 AA; 85704 MW; C26C9D6BB2D929A7 CRC64;

Query Match 80.0%; Score 44; DB 1; Length 770;
 Best Local Similarity 88.9%; Pred. No. 0.43;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQKLVFFAQ 10
 DB 685 HQKLVFFAE 693

RESULT 11
 G6PI_ECOLI STANDARD; PRT; 549 AA.

AC P11537;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
 DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
 DE PGI OR B4025 OR 25623 OR ECS5008.
 GN Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=JM101;
 RX MEDLINE=89364675; PubMed=2549364;
 RA Froman B.E., Tait R.C., Gottlieb L.D.;
 RT "Isolation and characterization of the phosphoglucose isomerase gene
 RT from Escherichia coli.";
 RL Mol. Gen. Genet. 217:126-131(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND PHYLOGENETIC STUDY.
 RC STRAIN=XL1 BLUE 2;
 RX MEDLINE=92277670; PubMed=1593646;
 RA Smith M.W., Doolittle R.F.;
 RT "Anomalous phylogeny involving the enzyme glucose-6-phosphate
 RT isomerase.";
 RL J. Mol. Evol. 34:544-545(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=94089392; PubMed=8265357;
 RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
 RA Daniels D.L.;
 RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the

RT region from 89.2 to 92.8 minutes.*;
 RL Nucleic Acids Res. 21:5408-5417(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206351;
 RA Perna N.T., Plunkett G. III, Burlant V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lim A., Dimailanta E.T., Potamoulsis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT *Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.*;
 RL Nature 409:529-533(2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / RMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kubara S., Shiba T., Hattori M., Shinagawa H.;
 RT *Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12.*;
 RL DNA Res. 8:11-22(2001).
 CC -!- CATALYTIC ACTIVITY: D-glucose 6-phosphate -> D-fructose 6-
 phosphate.
 CC -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X15196; CA33268.1; -
 DR EMBL: U00006; AAC43119.1; -
 DR EMBL: AE000476; AAC76995.1; -
 DR EMBL: AE005635; AAG59224.1; -
 DR EMBL: AP002568; BAB38431.1; -
 DR PIR: JS0142; NUC.
 DR EcoGene: EG10702; pgi.
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; PGI; 1.
 DR PRINTS: PR00662; G6PISOMERASE.
 DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; 1.
 KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
 FT ACT_SITE 386 386 BY SIMILARITY.
 FT ACT_SITE 514 514 BY SIMILARITY.
 FT CONFLICT 317 317 L -> V (IN REF. 1 AND 2).
 SQ SEQUENCE 549 AA; 61329 MW; 74AEDB670A068A01 CRC64;

 Query Match 74.5%; Score 41; DB 1; Length 549;
 Best Local Similarity 75.0%; Pred. No. 1.2;
 Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 HHQKLV--FFAQ 10
 DB 416 HHQKLLSNFFAQ 427

 RESULT 12
 ID G6PL_VIBCH STANDARD; PRT; 550 AA.
 AC Q9KUY4;
 DT 01-MAR-2002 (Rel. 41, Created)

DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
 DE isomerase) (PGI) (Phosphohexose isomerase) (PHI).
 OS Vibrio cholerae.
 GN NCBI_TaxID=666;
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT *DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae.*;
 RL Nature 406:477-483(2000).
 CC -!- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE -> FRUCTOSE 6-PHOSPHATE.
 CC -!- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE GPI FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AE004125; AAF93547.1; -
 DR TIGR: VC0374; -
 DR InterPro: IPR001672; G6P_Isomerase.
 DR Pfam: PF00342; PGI; 1.
 DR PRINTS: PR00662; G6PISOMERASE.
 DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
 DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; 1.
 KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
 FT ACT_SITE 387 387 BY SIMILARITY.
 FT ACT_SITE 515 515 BY SIMILARITY.
 SQ SEQUENCE 550 AA; 60690 MW; 5E38B0421C3A1B16 CRC64;

 Query Match 74.5%; Score 41; DB 1; Length 550;
 Best Local Similarity 75.0%; Pred. No. 1.2;
 Matches 9; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
 QY 1 HHQKLV--FFAQ 10
 DB 417 HHQKLLSNFFAQ 428

 RESULT 13
 ID MALQ_HAEIN STANDARD; PRT; 699 AA.
 AC P45176;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 4-alpha-glucanotransferase (EC 2.4.1.25) (Amylomaltase)
 DE (Disproportionating enzyme) (D-enzyme).
 GN MALQ OR H11356
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC STRAIN-RD / KW20 / ATCC 51907;
RX MEDLINE-95350630; PubMed-7342800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd."
RL Science 289:496-512(1995).
CC -1- CATALYTIC ACTIVITY: Transfers a segment of a (1,4)-alpha-D-glucan
CC to a new 4-position in an acceptor, which may be glucose or (1,4)-
CC alpha-D-glucan.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE DISPROPORTIONATING ENZYME FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U32815; AAC23003.1;
DR TIGR; H11356;
DR InterPro; IPR003385; 4A-glucanotrans.
DR Pfam; PF02446; 4A-glucanotrans; 1.
DR Transferase; Glycosyltransferase; Carbohydrate metabolism;
KW Complete proteome.
SQ SEQUENCE 699 AA; 80251 MW; 80D6E1D51EC2E1E9 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 699;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HHOKLVEFA 9
|||:||||
Db 349 HHKIQFFA 357

RESULT 14
G6PI_BUCAI
ID G6PI_BUCAI STANDARD; PRT; 549 AA.
AC P57636;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (Pgi) (Phosphohexose isomerase) (PHI).
GN PGI OR BU573.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TOKYO 1998;
RX MEDLINE-20445173; PubMed-10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT Buchnera sp. APS.;
RL Nature 407:81-86(2000).
CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate - D-fructose 6-
CC phosphate.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.

```

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP001119; BAB13263.1;
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 386 386 BY SIMILARITY.
FT ACT_SITE 514 514 BY SIMILARITY.
SQ SEQUENCE 549 AA; 63435 MW; 8DF547CE08382244 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 549;
Best Local Similarity 66.7%; Pred. No. 4.7;
Matches 8; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 1 HHOKLV--FFAQ 10
|||:||||
Db 416 HHMKLISNFFAQ 427

RESULT 15
G6PI_PASMU
ID G6PI_PASMU STANDARD; PRT; 549 AA.
AC Q9CNL2;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
DE isomerase) (Pgi) (Phosphohexose isomerase) (PHI).
GN PGI OR PM0416.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PM70;
RX MEDLINE-21145866; PubMed-11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -1- CATALYTIC ACTIVITY: GLUCOSE 6-PHOSPHATE - FRUCTOSE 6-PHOSPHATE.
CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF006077; AAK02500.1;
DR InterPro; IPR001672; G6P_Isomerase.
DR Pfam; PF00342; PGI; 1.
DR PRINTS; PR00662; G6PISOMERASE.
DR PROSITE; PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE; PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT ACT_SITE 387 387 BY SIMILARITY.
FT ACT_SITE 515 515 BY SIMILARITY.

```

SQ SEQUENCE 549 AA; 61437 MW; E6E4856927B93283 CRC64;

Query Match 59.1%; Score 38; DB 1; Length 549;
 Best Local Similarity 66.7%; Pred. No. 4.7;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 1 HHQKLV--FFAQ 10
 ||:|: |||
 Db 417 HHEKLLSNFFAQ 428

Search completed: July 18, 2002, 10:17:39
 Job time: 66 sec

GenCore version 4.5
 Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:13 ; Search time 25.17 Seconds
 (without alignments)
 68.731 Million cell updates/sec

Title: US-09-724-842-27
 Perfect score: 55
 Sequence: 1 HHQKLVFFAQ 10

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	94.5	28	Q9UCD1	Q9UCD1 homo sapien
2	52	94.5	30	Q9UCA9	Q9UCA9 homo sapien
3	52	94.5	33	Q9UC33	Q9UC33 homo sapien
4	52	94.5	82	P78438	P78438 homo sapien
5	52	94.5	82	Q16014	Q16014 homo sapien
6	52	94.5	82	Q16019	Q16019 homo sapien
7	52	94.5	82	Q16020	Q16020 homo sapien
8	52	94.5	97	Q13778	Q13778 homo sapien
9	52	94.5	534	Q93296	Q93296 gallus gall
10	52	94.5	569	Q9PVL1	Q9PVL1 gallus gall
11	52	94.5	693	Q98SG0	Q98SG0 xenopus lae
12	52	94.5	695	Q95KN7	Q95KN7 macaca fasc
13	52	94.5	695	Q60496	Q60496 cavia sp. p
14	52	94.5	695	Q9DGJ8	Q9DGJ8 gallus gall
15	52	94.5	747	Q91963	Q91963 xenopus. ap
16	52	94.5	751	Q9DGJ7	Q9DGJ7 gallus gall

17	52	94.5	770	6	Q9TUI0	Q9TUI0 sus scrofa
18	52	94.5	780	13	O73683	O73683 tetraodon f
19	50	90.9	695	13	Q98SF9	Q98SF9 xenopus lae
20	46	83.6	612	13	Q919E7	Q919E7 brachydanio
21	46	83.6	699	13	O57394	O57394 narke japon
22	46	83.6	738	13	Q90W28	Q90W28 brachydanio
23	44	80.0	79	11	O35463	O35463 cricetus
24	44	80.0	607	11	Q99K32	Q99K32 mus musculus
25	44	80.0	695	11	P97487	P97487 mus musculus
26	44	80.0	737	13	O93279	O93279 fugu rubrip
27	41	74.5	326	2	Q9K376	Q9K376 escherichia
28	41	74.5	326	2	Q9K328	Q9K328 escherichia
29	41	74.5	326	2	Q9K2T3	Q9K2T3 escherichia
30	41	74.5	326	2	Q9K2R7	Q9K2R7 escherichia
31	41	74.5	326	2	Q9K2Q3	Q9K2Q3 escherichia
32	41	74.5	326	2	Q9KH87	Q9KH87 escherichia
33	41	74.5	326	2	Q9KH85	Q9KH85 escherichia
34	41	74.5	326	2	Q9KH84	Q9KH84 escherichia
35	40	72.7	19	4	Q9UC8	Q9UC8 homo sapien
36	40	72.7	191	10	Q9SN52	Q9SN52 arabidopsis
37	40	72.7	584	5	Q900M8	Q900M8 plasmodium
38	38	69.1	272	16	P96882	P96882 mycobacteri
39	37	67.3	326	2	Q9KH86	Q9KH86 escherichia
40	37	67.3	364	2	Q93CU7	Q93CU7 shigella bo
41	37	67.3	626	16	Q9K185	Q9K185 neisseria m
42	37	67.3	635	16	Q9JSP1	Q9JSP1 neisseria m
43	37	67.3	1035	2	Q93E19	Q93E19 acinetobact
44	36	65.5	103	6	Q9XST6	Q9XST6 canis famil
45	36	65.5	152	11	Q9CUY7	Q9CUY7 mus musculus

ALIGNMENTS

RESULT 1

Q9UCD1 PRELIMINARY; PRT; 28 AA.

AC Q9UCD1;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE BETA-AMYLOID PEPTIDE (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=94045685; PubMed=8229004;

RA Vigo-Pelfrey C., Lee D., Keim P., Lieberburg I., Schenk D.B.;

RT "Characterization of beta-amyloid peptide from human cerebrospinal fluid."

RL J. Neurochem. 61:1965-1968(1993).

DR HSSP: P05067; IAMB.

SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match

Best Local Similarity 94.5%; Score 52; DB 4; Length 28;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
 |||||
 DB 13 HHQKLVFFAE 22

RESULT 2

Q9UCA9 PRELIMINARY; PRT; 30 AA.

AC Q9UCA9;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

```

DE BETA-AMYLOID PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient.";
RL Ann. Neurol. 35:245-246(1994).
DR HSP; P05067; IBA4.
SQ SEQUENCE 30 AA; 3391 MW; PF4167ABD081160A CRC64;

Query Match 94.5%; Score 52; DB 4; Length 30;
Best Local Similarity 90.0%; Pred. No. 0.0016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 13 HHQKLVFFAE 22

RESULT 3
O9UC33 PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSP; P05067; IBA4.
SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 94.5%; Score 52; DB 4; Length 33;
Best Local Similarity 90.0%; Pred. No. 0.0018;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 13 HHQKLVFFAE 22

RESULT 4
P78438 PRELIMINARY; PRT; 82 AA.
ID P78438;
AC P78438;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
GN APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1;
DR EMBL; M15532; AAA51564.1; JOINED.
DR EMBL; S45136; AAB23646.1;
DR HSP; P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9E42B813A070E CRC64;

Query Match 94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 29 HHQKLVFFAE 38

RESULT 5
Q16014 PRELIMINARY; PRT; 82 AA.
ID Q16014;
AC Q16014;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Demnan R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2;
DR HSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 30 HHQKLVFFAE 39

```

```

RESULT 6
Q16019 ID Q16019 PRELIMINARY; PRT; 82 AA.
AC Q16019;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61380; AAB26264.2; -.
DR HSSP; P05067; 1BA4.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

```

```

Query Match 94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HHQKLVFFAQ 10
| | | | | | | |
DB 30 HHQKLVFFAE 39

```

```

RESULT 7
Q16020 ID Q16020 PRELIMINARY; PRT; 82 AA.
AC Q16020;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYL0ID PEPTIDE (FRAGMENT).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Derman R.B., Rosenzwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
mutations on the processing of the beta-amyloid peptide precursor."
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S61383; AAB26265.2; -.
DR HSSP; P05067; 1BA4.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

```

```

Query Match 94.5%; Score 52; DB 4; Length 82;
Best Local Similarity 90.0%; Pred. No. 0.0045;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HHQKLVFFAQ 10
| | | | | | | |
DB 30 HHQKLVFFAE 39

```

```

RESULT 8
Q13778 ID Q13778 PRELIMINARY; PRT; 97 AA.
AC Q13778;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE AMYL0ID PROTEIN (AD-AP) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87120328; PubMed=3810169;
RA Goldgaber D., Lerman M.I., McBride O.W., Saffioti U., Gajdusek D.C.;
RT "Characterization and chromosomal localization of a cDNA encoding
RT brain amyloid of Alzheimer's disease."
RL Science 235:877-880(1987).
DR EMBL; M15533; AAA35540.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYL0ID4.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE474E CRC64;

```

```

Query Match 94.5%; Score 52; DB 4; Length 97;
Best Local Similarity 90.0%; Pred. No. 0.0053;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HHQKLVFFAQ 10
| | | | | | | |
DB 11 HHQKLVFFAE 20

```

```

RESULT 9
Q93296 ID Q93296 PRELIMINARY; PRT; 534 AA.
AC Q93296;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYL0ID PROTEIN (FRAGMENT).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons."
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL; AF042098; AAC25052.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR PRINTS; PR00203; AMYL0ID4.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E65D4C92 CRC64;

```

```

Query Match 94.5%; Score 52; DB 13; Length 534;
Best Local Similarity 90.0%; Pred. No. 0.031;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HHQKLVFFAQ 10

```



```

Db 448 HHQKLVFFAE 457
|||||
RESULT 10
Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RL Neurochem. Int. 0:0-0(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSP; P05067; IBA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;

Query Match 94.5%; Score 52; DB 13; Length 569;
Best Local Similarity 90.0%; Pred. No. 0.033;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
|||||
Db 484 HHQKLVFFAE 493

RESULT 11
Q98SGO PRELIMINARY; PRT; 693 AA.
AC Q98SGO
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSP; P05067; IHZ3.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.

```

```

KW Signal. 18
FT SIGNAL 18
SQ SEQUENCE 693 AA; 78568 MW; CAF1DF655C1AB653 CRC64;

Query Match 94.5%; Score 52; DB 13; Length 693;
Best Local Similarity 90.0%; Pred. No. 0.04;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
|||||
Db 607 HHQKLVFFAE 616

RESULT 12
Q95KN7 PRELIMINARY; PRT; 695 AA.
AC Q95KN7
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciniae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CEREBELLUM;
RX MEDLINE-91273117; PubMed-1905108;
RA Podlasky M.B., Toland D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -.
FT SIGNAL 17
FT CHAIN 597 636
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 94.5%; Score 52; DB 6; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.04;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
|||||
Db 609 HHQKLVFFAE 618

RESULT 13
Q60496 PRELIMINARY; PRT; 695 AA.
AC Q60496
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-97236426; PubMed-9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSP; P05067; IBA4.

```

```

DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
SQ SEQUENCE 695 AA; 78701 MW; 5196AOC4017F16AB CRC64;

Query Match          94.5%; Score 52; DB 11; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.04;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 609 HHQKLVFFAE 618

RESULT 14
Q9DGJ8 PRELIMINARY; PRT; 695 AA.
AC Q9DGJ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Sarasa M., Rodolosse A., Sorribas V.;
RT "Cloning of full-length chicken beta-amyloid precursor protein
RT isoforms ";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289218; AAG00593.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match          94.5%; Score 52; DB 13; Length 695;
Best Local Similarity 90.0%; Pred. No. 0.04;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 609 HHQKLVFFAE 618

RESULT 15
Q91963 PRELIMINARY; PRT; 747 AA.
ID Q91963
AC Q91963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE APP747.
DE APP747.
GN APP747.
OS Xenopus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae.
OX NCBI_TaxID=8353;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93129227; PubMed=1282805;

```

```

RA Okado H., Okamoto H.;
RT "A Xenopus homologue of the human beta-amyloid precursor protein:
RT developmental regulation of its gene expression.";
RL Biochem. Biophys. Res. Commun. 189:1561-1568(1992).
DR EMBL; S52417; AAB24853.1; -.
DR HSSP; P05067; 1H23.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.
DR SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Serine protease inhibitor.
SQ SEQUENCE 747 AA; 84893 MW; A75E81885681D948 CRC64;

```

```

Query Match          94.5%; Score 52; DB 13; Length 747;
Best Local Similarity 90.0%; Pred. No. 0.04;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HHQKLVFFAQ 10
DB 661 HHQKLVFFAE 670

```

```

Search completed: July 18, 2002, 10:17:22
Job time: 69 sec

```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:13:48 ; Search time 13.06 Seconds
(without alignments)
18.703 Million cell updates/sec

Title: US-09-724-842-27
Perfect score: 55
Sequence: 1 HHOKLVFFAQ 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCFUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	28	4	US-09-388-890-12
2	55	100.0	40	1	US-08-304-585-8
3	55	100.0	63	1	US-08-462-859A-3
4	55	100.0	63	1	US-08-123-659A-3
5	55	100.0	63	1	US-08-464-247A-3
6	55	100.0	63	1	US-08-464-248A-3
7	55	100.0	99	3	US-08-339-708A-6
8	52	94.5	15	2	US-08-612-785B-37
9	52	94.5	17	4	US-09-264-709A-2
10	52	94.5	26	1	US-08-304-585-7
11	52	94.5	28	1	US-08-346-849-4
12	52	94.5	28	1	US-08-302-808-7
13	52	94.5	28	2	US-08-605-090-2
14	52	94.5	28	2	US-08-986-948-7
15	52	94.5	28	2	US-08-293-284A-4
16	52	94.5	28	2	US-08-461-216-2
17	52	94.5	28	4	US-09-388-890-2
18	52	94.5	28	4	US-09-388-890-3
19	52	94.5	28	4	US-09-388-890-4
20	52	94.5	28	4	US-09-388-890-5
21	52	94.5	28	4	US-09-388-890-6
22	52	94.5	28	4	US-09-388-890-7
23	52	94.5	28	4	US-09-388-890-8
24	52	94.5	28	4	US-09-388-890-13
25	52	94.5	28	4	US-09-388-890-14
26	52	94.5	28	4	US-09-264-709A-1
27	52	94.5	28	4	US-08-723-661B-2

28	52	94.5	30	2	US-08-609-090-3	Sequence 3, Appl1
29	52	94.5	33	2	US-08-609-090-4	Sequence 4, Appl1
30	52	94.5	35	1	US-08-304-585-6	Sequence 6, Appl1
31	52	94.5	35	2	US-08-612-785B-36	Sequence 36, Appl1
32	52	94.5	35	2	US-08-612-785B-40	Sequence 40, Appl1
33	52	94.5	35	2	US-08-609-090-6	Sequence 6, Appl1
34	52	94.5	36	1	US-08-302-808-1	Sequence 1, Appl1
35	52	94.5	38	2	US-07-737-371E-68	Sequence 68, Appl1
36	52	94.5	38	2	US-08-986-948-1	Sequence 1, Appl1
37	52	94.5	38	2	US-08-304-585-5	Sequence 5, Appl1
38	52	94.5	39	1	US-08-302-808-2	Sequence 2, Appl1
39	52	94.5	39	2	US-08-609-090-7	Sequence 7, Appl1
40	52	94.5	39	2	US-08-682-245A-1	Sequence 1, Appl1
41	52	94.5	39	2	US-08-986-948-2	Sequence 2, Appl1
42	52	94.5	40	1	US-07-744-767A-1	Sequence 1, Appl1
43	52	94.5	40	1	US-08-235-400-2	Sequence 2, Appl1
44	52	94.5	40	1	US-08-476-464A-2	Sequence 2, Appl1
45	52	94.5	40	1	US-08-476-464A-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-388-890-12
; Sequence 12, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E220 B(1-28) peptide of amyloid B protein
US-09-388-890-12

Query Match 100.0%; Score 55; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
| | | | | | | |
Db 13 HHQKLVFFAQ 22

RESULT 2

US-08-304-585-8
; Sequence 8, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyn, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-304-585-8

Query Match 100.0%; Score 55; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
| | | | | | | |
Db 13 HHQKLVFFAQ 22

RESULT 3

US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company

STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,859A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 55; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
| | | | | | | |
Db 22 HHQKLVFFAQ 31

RESULT 4

US-08-123-659A-3
; Sequence 3, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/123,659A
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELEPHONE: (518)475-0611

TELEFAX: (518)475-0619
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-123-659A-3

Query Match 100.0%; Score 55; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 22 HHQKLVFFAQ 31

RESULT 5

US-08-464-247A-3
Sequence 3, Application US/08464247A
Patent No. 5693478

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.

APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
STREET: One Campus Drive

CITY: Parsippany
STATE: New Jersey

COUNTRY: United States
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 63 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-464-247A-3

Query Match 100.0%; Score 55; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 22 HHQKLVFFAQ 31

RESULT 6

US-08-464-248A-3
Sequence 3, Application US/08464248A
Patent No. 5703209

GENERAL INFORMATION:
APPLICANT: Jacobsen, J. S.

APPLICANT: Vitek, M. P.
TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of

TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
TITLE OF INVENTION: of B-Amyloid Peptide
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza

CITY: Wayne
STATE: New Jersey

COUNTRY: United States
ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088

REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:

TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 63 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-464-248A-3

Query Match 100.0%; Score 55; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.00061;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 22 HHQKLVFFAQ 31

RESULT 7

US-08-339-708A-6

Sequence 6, Application US/08339708A
Patent No. 6037521

GENERAL INFORMATION:
APPLICANT: Sato, Masahiro

APPLICANT: Takashi, Kobayashi
APPLICANT: Tada, No. 6037521hiro

APPLICANT: Shoji, Mikio
APPLICANT: Kawarabayashi, Takeshi

TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500

CITY: Washington
STATE: D.C.

COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,708A
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 306026/93
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0159
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-708A-6

Query Match 100.0%; Score 55; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 13 HHQKLVFFAQ 22

RESULT 8
US-08-612-785B-37
Sequence 37, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
APPLICATION NUMBER:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 94.5%; Score 52; DB 2; Length 15;
Best Local Similarity 90.0%; Pred. No. 0.00051;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 3 HHQKLVFFAE 12

RESULT 9
US-09-264-709A-2
Sequence 2, Application US/09264709A
Patent No. 6320024
GENERAL INFORMATION:
APPLICANT: Roberts, Eugene
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
TITLE OF INVENTION: Improve the Quality of Life
FILE REFERENCE: 2124-310
CURRENT APPLICATION NUMBER: US/09/264,709A
CURRENT FILING DATE: 1999-03-09
PRIOR APPLICATION NUMBER: 08/797,782
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-264-709A-2

Query Match 94.5%; Score 52; DB 4; Length 17;
Best Local Similarity 90.0%; Pred. No. 0.00058;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
DB 2 HHQKLVFFAE 11

RESULT 10
US-08-304-585-7
Sequence 7, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Magglo, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110,00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-304-585-7

```

Query Match 94.5%; Score 52; DB 1; Length 26;
 Best Local Similarity 90.0%; Pred. No. 0.0009;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 HHQKLVFFAQ 10
    |||
DB 4 HHQKLVFFAE 13

```

```

RESULT 11
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-346-849-4

```

Query Match 94.5%; Score 52; DB 1; Length 28;
 Best Local Similarity 90.0%; Pred. No. 0.00098;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 HHQKLVFFAQ 10
    |||
DB 13 HHQKLVFFAE 22

```

```

RESULT 12
US-08-302-808-7
; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal

```


ORIGINAL SOURCE:
US-08-302-808-7

Query Match 94.5%; Score 52; DB 1; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
Db 13 HHQKLVFFAE 22

RESULT 13

US-08-609-090-2
Sequence 2, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-2

Query Match 94.5%; Score 52; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
Db 13 HHQKLVFFAE 22

RESULT 14

US-08-986-948-7
Sequence 7, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro

APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-986-948-7

Query Match 94.5%; Score 52; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
Db 13 HHQKLVFFAE 22

RESULT 15

US-08-293-284A-4
Sequence 4, Application US/08293284A
Patent No. 5955343
GENERAL INFORMATION:
APPLICANT: Holmes, Todd
APPLICANT: Zhang, Shuangang
APPLICANT: Rich, Alexander

```

; APPLICANT: DIPERSIO, C. Michael
; APPLICANT: LOCKSHIN, Curtis
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSER: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: TWO Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/293,284A
; FILING DATE: 22-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOK, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-293-284A-4

```

```

Query Match          94.5%; Score 52; DB 2; Length 28;
Best Local Similarity 90.0%; Pred. No. 0.00098;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
Db 13 HHQKLVFFAE 22

```

Search completed: July 18, 2002, 10:16:29
Job time: 161 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:39 ; Search time 29.95 seconds
(without alignments)
37.086 Million cell updates/sec

Title: US-09-724-842-27

Perfect score: 10

Sequence: 1 HHQKLVFFAQ 10

Scoring table: OLIGO ;
Gapop 60.0 , Capext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574
(without alignments)

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_032802.*

1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	100.0	10	22	AA82641
2	10	100.0	28	17	AAW01414
3	10	100.0	28	22	AA835600
4	10	100.0	35	22	AA891803
5	10	100.0	35	22	AA891830
6	10	100.0	40	19	AAW47232
7	10	100.0	40	19	AAW47232
8	10	100.0	53	15	AA855697
9	10	100.0	63	18	AAW26511
10	10	100.0	63	18	AAW26391
11	10	100.0	63	19	AAW4746
				19	AAW42975

12	10	100.0	99	16	AA874695	Beta-amyloid precu
13	9	90.0	9	22	AA848493	Antifibrillogenic
14	9	90.0	10	22	AA846224	Human APP derived
15	9	90.0	10	22	AA846225	Human APP derived
16	9	90.0	15	20	AA893558	Beta-amyloid pepti
17	9	90.0	17	15	AA834703	Beta-amyloid fragm
18	9	90.0	17	22	AA891774	Amyloid beta-prote
19	9	90.0	17	22	AA891807	Amyloid beta-prote
20	9	90.0	17	22	AA848346	Beta-amyloid anti
21	9	90.0	18	21	AA810963	Beta-amyloid precu
22	9	90.0	19	18	AAW18882	ADANS-beta-amyloi
23	9	90.0	19	18	AAW18881	Trp-Beta-amyloid p
24	9	90.0	19	22	AA846201	Human APP A-beta 1
25	9	90.0	19	22	AA849097	Human amyloid beta
26	9	90.0	21	20	AA830941	Human secretase SE
27	9	90.0	24	15	AA825669	Alzheimer's diseas
28	9	90.0	26	19	AAW47229	Beta-amyloid pepti
29	9	90.0	26	20	AA833408	Human amyloidogen1
30	9	90.0	27	20	AA833409	Human amyloidogen1
31	9	90.0	28	8	AA870594	Sequence of Alzhei
32	9	90.0	28	10	AA890381	Synthetic A4 amyo
33	9	90.0	28	15	AA834702	Beta-amyloid fragm
34	9	90.0	28	15	AA860368	Beta-amyloid (1-28
35	9	90.0	28	16	AA864170	A4-O(1-28) a parti
36	9	90.0	28	16	AA864171	A4-P(1-28) a parti
37	9	90.0	28	16	AA864172	A4-B(1-28) a parti
38	9	90.0	28	16	AA864164	Generic beta amyo
39	9	90.0	28	17	AAW01413	Beta/A4-amyloid pe
40	9	90.0	28	20	AA839805	Synthetic amyloid
41	9	90.0	28	20	AA81467	Amyloid beta-prote
42	9	90.0	28	22	AA891783	Amyloid beta-prote
43	9	90.0	28	22	AA891789	Amyloid beta-prote
44	9	90.0	28	22	AA891800	Amyloid beta-prote
45	9	90.0	28	22	AA891816	Amyloid beta-prote

ALIGNMENTS

RESULT 1
AA82641
ID AA82641 standard; Peptide; 10 AA.
AC AA82641;
XX
XX
DT 02-OCT-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
XX Alzheimer's disease; amyloidosis; amyloid-related disease;
KW vaccine; therapy; antigen.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT Misc-difference 1..10
FT /note= "all D-form residues"
XX
XX WO200139796-A2.
XX
XX 07-JUN-2001.
XX
XX 29-NOV-2000; 2000WO-CA01413.
XX
XX 29-NOV-1999; 99US-0168594.
XX
XX 28-NOV-2000; 2000US-0724842.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Challifour R, Hebert L, Kong X, Gervais F;
XX WPI; 2001-441458/47.
XX

PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, e.g. as
 PT vaccine, which elicits production of antibodies to prevent
 XX fibrillogenesis and associated cellular toxicity -
 XX
 PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for
 CC use in preparing vaccines for preventing or treating Alzheimer's
 CC disease and other amyloid related disorders in humans. It is based
 CC on a portion of amyloid-beta peptide (see AAB82622), and may be
 CC modified by removing or inserting 1 or more amino acid residues, or
 CC by substituting 1 or more amino acid residues with other amino acid
 CC residues or non-amino acid fragments. Vaccines of the invention
 CC are produced using 'non-self' peptides synthesised from the
 CC unnatural D-configuration amino acids to avoid the drawbacks of
 CC 'self' proteins. The all-D peptides need not be aggregated to be
 CC operative or immunogenic. They preferably interact with at
 CC least 1 region of an amyloid protein, e.g. the beta-sheet region
 CC or GAG-binding site region, the amyloid-beta peptide, or their
 CC immunogenic fragments, protein conjugates, immunogenic derivative
 CC peptides and immunogenic peptidomimetics. Examples include all-D
 CC peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7,
 CC 10-15, 16-21 and 36-42 of the amyloid-beta peptide and the all-D
 CC derivative peptides given in AAB82623-64. The vaccine elicits a
 CC preferential TH-2 or TH-1 response, preventing fibrillogenesis and
 CC associated cellular toxicity. The amyloid related diseases may be
 CC localised amyloidosis, e.g. diabetes type II, neurodegenerative
 CC diseases, e.g. bovine spongiform encephalitis, Creutzfeldt-Jakob
 CC disease, scrapie, cerebral amyloid angiopathy, and prion protein
 CC related disorders, or systemic amyloidosis associated with chronic
 CC infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and
 CC systemic amyloidosis found in long-term haemodialysis patients.

XX Sequence 10 AA;

Query Match 100.0%; Score 10; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.1e-05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
 |||||
 Db 1 hhqklvffaq 10

RESULT 2
 AAW01414
 ID AAW01414 standard; Protein; 28 AA.

XX AAW01414;

XX 20-JAN-1997 (first entry)

DE Beta/A4-amyloid peptide residues 1-28 Dutch.

XX Beta/A4-amyloid peptide; tissue plasminogen activator; Dutch;
 KW Alzheimer's disease; stimulation; investigation; pathogenesis;
 KW hereditary cerebral haemorrhage with amyloidosis-Dutch type;
 KW control; cerebral amyloid angiopathy; cerebral; haemorrhage;
 KW hemorrhage.

XX Homo sapiens.

XX Key Location/Qualifiers
 PH Misc-difference 22

FT /note- "wild type Glu substd. with Gln"

PN WO9615799-A1.

XX 30-MAY-1996.

XX

PF 22-NOV-1995; 95WO-US15007.
 XX
 PR 22-NOV-1994; 94US-0347144.
 XX
 PA (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 PI Anderson S;

XX WPI; 1996-268332/27.

PT Use of agents which bind beta-amyloid peptide - for diagnosis,
 PT prevention and treatment of vascular damage caused by amyloid
 PT deposits, partic. in haemorrhaging and Alzheimer's disease
 XX
 PS Example 1; Fig 1; 52pp; English.

XX To investigate the effects of beta-amyloid peptide (BAP) on

CC tissue plasminogen activator (t-PA) 3 synthetic peptides were used.
 CC One peptide contained 42 amino acids and corresp. to the full
 CC length BAP (AAR95248). The other 2 peptides (AAR95249 and 50) contained
 CC the 28 N-terminal residues of the BAP found in Alzheimer's disease
 CC and hereditary cerebral haemorrhage with amyloidosis-Dutch type
 CC (HCHWA-D), respectively. In an assay to determine the effect of
 CC the peptides on t-PA activation, each peptide (kapp) values of
 CC gave 1st order rate constant of activation (kapp) values of
 CC 13.4, 13.9 and 14.5, respectively, compared to 1.7 and 7.8 for null
 CC and fibrinogen controls. The results demonstrate that the BAP are
 CC able to stimulate t-PA activity in vitro, which is significant in
 CC that it provides a means for investigating and controlling the
 CC pathogenesis of Alzheimer's disease, HCHWA-D and cerebral amyloid
 CC angiopathy related cerebral haemorrhage.

XX Sequence 28 AA;

Query Match 100.0%; Score 10; DB 17; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
 |||||
 Db 13 hhqklvffaq 22

RESULT 3
 AAB35600
 ID AAB35600 standard; peptide; 28 AA.

XX AAB35600;

XX 15-FEB-2001 (first entry)

XX Human clone E22Q B(1-28) amyloid B peptide.

XX Beta-amyloid; amyloid deposit; Alzheimer's disease; thrombolytic therapy;
 KW acute cardiovascular disease; therapy.

XX Homo sapiens.

XX US6136548-A.

PD 24-OCT-2000.

XX 02-SEP-1999; 99US-0388890.

XX 26-JUL-1996; 96US-0686959.

XX 22-NOV-1994; 94US-0347144.

XX 22-NOV-1995; 95WO-US15007.

XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.

XX Anderson S;

DR WPI; 2001-030939/04.
XX Identifying mutant tissue-type plasminogen activator (t-PA) for
PT improving thrombolytic therapy or treating vascular hemorrhaging, by
PT determining whether t-PA binds to fibrin but not to a beta amyloid
PT peptide
XX
XX Example 3; Column 26; 23pp; English.
XX
XX The present invention describes a method for identifying mutant
CC derivatives of tissue-type plasminogen activator, which involves
CC determining whether or not they bind to beta-amyloid peptides and fibrin.
CC Mutants will only bind to the latter. These mutants are useful in
CC improved thrombolytic therapies, in the treatment of Alzheimer's disease
CC and in the treatment of acute cardiovascular disease, which may be caused
CC by myocardial infarction, stroke, ischaemia and pulmonary embolism.
XX
XX Sequence 28 AA;

Query Match 100.0%; Score 10; DB 22; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
Db 13 hhqklvffaq 22

RESULT 4
AAB91803
ID AAB91803 standard; Peptide; 35 AA.

AC AAB91803;
DT 22-JUN-2001 (first entry)
XX
XX Amyloid beta-protein fragment peptide SEQ ID NO:979.
DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200069900-A2.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR
XX 10-SEP-1999; 99US-0153406.
PR
XX 15-OCT-1999; 99US-0159783.
XX

PA (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI
XX WPI; 2001-112059/12.
DR
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 514; 733pp; English.
PS
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
XX

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
XX Sequence 35 AA;

Query Match 100.0%; Score 10; DB 22; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFAQ 10
Db 8 hhqklvffaq 17

RESULT 5
AAB91830
ID AAB91830 standard; Peptide; 35 AA.

AC AAB91830;
DT 22-JUN-2001 (first entry)
XX
XX Amyloid beta-protein fragment peptide SEQ ID NO:1006.
DE
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200069900-A2.
PN
XX 23-NOV-2000.
PD
XX 17-MAY-2000; 2000WO-US13576.
PF
XX 17-MAY-1999; 99US-0134406.
PR
XX 10-SEP-1999; 99US-0153406.
PR
XX 15-OCT-1999; 99US-0159783.
XX

PA (CONJ-) CONJUCHEM INC.
XX
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
PI
XX WPI; 2001-112059/12.
DR
XX Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
PT
XX
XX Disclosure; Page 524; 733pp; English.
PS
XX The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 35 AA;

Query Match 100.0%; Score 10; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
 |||||
 Db 8 hhqklvffaq 17

RESULT 6
 AAW47232
 ID AAW47232 standard; peptide; 40 AA.
 AC AAW47232;
 XX
 XX 22-MAY-1998 (first entry)
 DT
 XX Beta-amyloid peptide fragment.
 DE
 XX Screening assay: beta-amyloid peptide; treatment;
 KW amyloidosis disease; Alzheimer's disease.
 XX Homo sapiens.
 OS
 XX US5721106-A.
 PN
 XX 24-FEB-1998.
 PD
 XX 12-SEP-1994; 94US-0304585.
 PF
 XX 12-SEP-1994; 94US-0304585.
 PR
 XX 13-AUG-1991; 91US-0744767.
 XX
 XX (HARD) HARVARD COLLEGE.
 PA (MINU) UNIV MINNESOTA.
 XX
 XX Maggio JE, Mantyh PW;
 PI WPI; 1998-168404/15.
 DR
 XX New in vitro screening assay for Alzheimer's disease drugs -
 PT comprises assessing binding of labelled beta-amyloid peptide to silk
 PT sample
 XX
 XX Disclosure; Columns 31-32; 36pp; English.

PS The present sequence was used in the development of a novel in
 CC vitro screening assay for agents capable of affecting the
 CC deposition of beta-amyloid peptide (BAP) on tissue. The method
 CC comprises contacting a silk sample with labelled BAP, optionally
 CC in the presence of a test agent, detecting the amount of label
 CC bound to the silk and assessing the effect of the agent on the
 CC deposition of BAP. Agents that inhibit binding of BAP to silk are
 CC potentially useful for treating amyloidosis diseases, especially
 CC Alzheimer's disease.
 XX
 SQ Sequence 40 AA;

Query Match 100.0%; Score 10; DB 19; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 HHQKLVFFAQ 10
 |||||
 Db 13 hhqklvffaq 22

RESULT 7
 AAR55697
 ID AAR55697 standard; Protein; 53 AA.
 XX
 AC AAR55697;
 XX
 XX 29-DEC-1994 (first entry)
 DT
 XX Sequence of unidentified protein sequence ID number 22.
 DE
 XX Amyloid precursor protein; APP; plaque; beta/A4; Alzheimers;
 KW transgene; ss.
 KW
 XX Synthetic.
 OS
 XX WO9412627-A.
 PN
 XX 09-JUN-1994.
 PD
 XX 24-NOV-1993; 93WO-US11480.
 PF
 XX 25-NOV-1992; 92US-0989850.
 PR
 XX 09-NOV-1993; 93US-0149222.
 XX
 XX (CEPH-) CEPHALON INC.
 PA
 XX Howland DS, Scott RW;
 PI WPI; 1994-200256/24.
 DR
 XX Transgenic animal model for Alzheimer's disease - contains
 PT transgene encoding amyloid protein under transcriptional control
 PT of synapsin gene promoter
 XX
 XX Example; Page 55; 94pp; English.

PS There was no apparent reference to sequence ID numbers 20, 21 or 22
 CC in the specification. The specification describes a transgenic
 CC animal model for Alzheimer's disease. A transgenic animal
 CC harbouring a transgene coding for an amyloid protein under the
 CC control of a promoter is claimed. The amyloid protein can be
 CC APP695, APP751 or APP770. The coding sequence may contain a
 CC mutation, including the hereditary cerebral haemorrhage with
 CC amyloidosis - Dutch type (HCHWA-DT) and familial Alzheimer's
 CC disease (FAD). Perhaps SQ IDs 20-22 corresp. to wt, HCHWA-DT
 CC and FAD?
 XX
 SQ Sequence 53 AA;

Query Match 100.0%; Score 10; DB 15; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.0002;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFAQ 10
 |||||
 Db 17 hhqklvffaq 26

RESULT 8
 AAW26511
 ID AAW26511 standard; Peptide; 63 AA.
 XX
 AC AAW26511;
 XX
 XX 06-JAN-1998 (first entry)
 DT

DE APP-REP 751 [BAP E22Q] peptide.
 XX Amyloid precursor protein; APP; APP 751 isoform; deletion; substrate P;
 KW epitope; Met-enkephalin; detection; secretase; beta-amyloid protein; BAP;
 KW Alzheimer's disease; cleavage.
 XX Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Cleavage-site 25..26
 FT /note= "secretase cleavage site"
 FT Misc-difference 31
 FT /note= "Glu to Gln change from wild type sequence"
 FT
 FN US5693478-A.
 FN
 PD 02-DEC-1997.
 XX
 XX 05-JUN-1995; 95US-0464247.
 XX
 XX 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 PR 05-JUN-1995; 95US-0464247.
 XX
 XX (AMCY) AMERICAN CYANAMID CO.
 XX
 XX Jacobsen JS, Vitek MP;
 XX WPI; 1998-031744/03.
 DR
 XX Amyloid precursor mutelin reporter molecule assay containing antibody
 FT recognised marker - used to study pathways associated with
 FT Alzheimer's disease
 XX
 XX Disclosure; Fig 5A; 84pp; English.
 XX
 XX This sequence represent the beta-amyloid protein sequence from the
 CC construct APP-REP751 [BAP E22Q]. The mutant sequence can be used in a
 CC method to study secretase and beta-amyloid protein (BAP)-generating
 CC pathways associated with Alzheimer's disease by studying proteolytic
 CC cleavage of the reporter polypeptides (e.g. AAW44744 and AAW44745).
 XX
 SQ Sequence 63 AA;
 Query Match 100.0%; Score 10; DB 19; Length 63;
 Best Local Similarity 100.0%; Pred. NO. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFAQ 10
 Db 22 hhqklvffaq 31
 |||||
 RESULT 11
 AAW42975
 ID AAW42975 standard; peptide; 63 AA.
 XX
 XX AAW42975;
 XX
 XX 01-MAY-1998 (first entry)
 DT
 XX
 XX Beta-amyloid peptide (BAP) E22Q.
 DE
 XX Beta-amyloid peptide; BAP; extracellular BAP plaque; amyloidosis;
 KW cerebrovascular deposit; Alzheimers disease; Downs syndrome;
 KW Dutch origin; amyloid precursor protein; APP; secretase; BAP aggregation;
 KW abnormal proteolytic cleavage; hereditary cerebral haemorrhage.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH

FT Domain 38..61
 FT /note= "putative transmembrane domain"
 FT Misc_feature 22
 FT /label= E22Q
 FT /note= "wild type Glu replaced with Gln"
 XX
 XX US5703209-A.
 XX
 XX 30-DEC-1997.
 PD
 XX 05-JUN-1995; 95US-0464248.
 XX
 XX 20-SEP-1993; 93US-0123659.
 PR 01-MAY-1992; 92US-0877675.
 PR
 XX (AMCY) AMERICAN CYANAMID CO.
 PA
 XX Jacobsen JS, Vitek MP;
 XX WPI; 1998-076482/07.
 DR
 XX Amyloid precursor protein fusion polypeptides - comprising APP
 FT fragment and marker, useful for research and drug screening
 FT
 XX Disclosure; Fig 5A; 84pp; English.
 PS
 XX
 XX The present sequence represents a beta-amyloid peptide (BAP) with a
 CC E22Q mutation. Abnormal accumulation of extracellular BAP in plaques
 CC and cerebrovascular deposits is characteristic in brains of individuals
 CC suffering from Alzheimers disease and Downs syndrome. BAP is a poorly
 CC soluble, self-aggregating protein which is derived from a larger amyloid
 CC precursor protein (APP). APP is expressed as an integral membrane
 CC protein, and is cleaved by secretase, between BAP 16lys and 17Leu.
 CC Cleavage at this site precludes amyloidogenesis and results in the
 CC release of the amino-terminal APP fragment. The E22Q mutation in BAP is
 CC found within the APP of patients with hereditary cerebral haemorrhage
 CC with amyloidosis of Dutch origin, and may be due to an alteration in the
 CC rate of BAP aggregation. APP can be used as a substrate for studying
 CC abnormal proteolytic cleavage which results in the release of BAP, and
 CC also to screen for drugs that will inhibit such cleavage.
 XX
 SQ Sequence 63 AA;
 Query Match 100.0%; Score 10; DB 19; Length 63;
 Best Local Similarity 100.0%; Pred. NO. 0.00023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFAQ 10
 Db 22 hhqklvffaq 31
 |||||
 RESULT 12
 AAR74695
 ID AAR74695 standard; Peptide; 99 AA.
 XX
 XX AAR74695;
 AC
 XX
 XX 11-NOV-1995 (first entry)
 DT
 XX
 XX Beta-amyloid precursor protein mutant C-terminal peptide.
 DE
 XX Human; beta-amyloid precursor protein mutant; C-terminal peptide;
 KW gene transfer; transgenic animal; Alzheimer disease model;
 KW gene therapy.
 KW
 XX Homo sapiens.
 OS
 XX EP653154-A.
 PN
 XX 17-MAY-1995.
 PD
 XX

PF 07-NOV-1994; 94EP-0117512.
 XX
 PR 12-NOV-1993; 93JP-0306026.
 XX
 PA (FARH) HOECHST JAPAN LTD.
 PA (FARH) HOECHST JAPAN KK.
 XX
 PI Kawarabayashi T, Kobayashi T, Sato M, Shoji M, Tada N;
 XX
 DR WPI; 1995-180492/24.
 DR N-PSDB; AAQ8697.
 XX
 XX Transgenic animal model for Alzheimer's disease - contains DNA encoding
 PT part of beta-amyloid precursor protein in a gene construct designed for
 PT over-expression in various cell types
 XX
 XX Claim 2; Page 13; 32pp; English.
 XX
 CC The sequence represents a human brain beta-amyloid precursor protein
 CC (APP) C-terminal peptide. The peptide is a Gln-22 mutant of
 CC AAR74694. DNA encoding the peptide may be transferred, along
 CC with a signal peptide (e.g. AAR74693) gene into somatic and germ
 CC cells of a non-human mammal, and the resulting transgenic animal
 CC may be used as a model for Alzheimer disease (AD). The animal
 CC model exhibits symptoms similar to AD, producing large quantities
 CC of APP C-terminal peptide, death of neuron cells in pyramidal
 CC cells at cerebral amyloid regions, increases in glial cells and
 CC deposition of abnormally phosphorylated tau protein. The animal
 CC model may be used to develop new therapies for AD, including
 CC gene therapy strategies.
 XX
 XX Sequence 99 AA;
 SQ
 Query Match 100.0%; Score 10; DB 16; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFFAQ 10
 Db 13 hhqklvffaq 22
 RESULT 13
 AAB48493
 ID AAB48493 standard; Peptide; 9 AA.
 AC
 XX AAB48493;
 XX
 DT 02-MAR-2001 (first entry)
 XX
 DE Antifibrillogenic peptide #20.
 XX
 KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 9
 FT /note= "C-terminal amide"
 XX
 PN WO200068263-A2.
 PD 16-NOV-2000.
 XX
 XX 04-MAY-2000; 2000WO-CA00515.
 XX
 XX 05-MAY-1999; 99US-0132592.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 WPI; 2001-032104/04.
 DR
 XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Figure 19; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

PI Chalifour R, Gervais F, Gupta A;
 XX
 DR WPI; 2001-031852/04.
 XX
 PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic -
 XX
 XX Claim 7; Page 25; 46pp; English.
 XX
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are
 CC therefore useful for treating amyloidosis disorders such as Alzheimer's
 CC disease. Peptides AAB48474-B48496 were identified from the
 CC glycosaminoglycan binding region and the prot-prot interaction region of
 CC the human amyloid protein.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 90.0%; Score 9; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHOKLVFFA 9
 Db 1 hhqklvffa 9
 RESULT 14
 AAB46224
 ID AAB46224 standard; peptide; 10 AA.
 AC
 XX AAB46224;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human APP derived immunogenic peptide #20.
 XX
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200072880-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 26-MAY-2000; 2000WO-US14810.
 XX
 PR 28-MAY-1999; 99US-0322289.
 XX
 XX (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 WPI; 2001-032104/04.
 DR
 XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX
 PS Disclosure; Figure 19; 143pp; English.
 XX
 CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent

CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX
 SQ Sequence 10 AA;

Query Match 90.0%; Score 9; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFA 9
 |||||
 DB 2 hhqklvffa 10

RESULT 15

AAB46225

ID AAB46225 standard; peptide; 10 AA.

AC AAB46225;

DT 04-APR-2001 (first entry)

XX Human APP derived immunogenic peptide #21.

XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

XX Homo sapiens.

XX WO200072880-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US14810.

XX 28-MAY-1999; 99US-0322289.

XX (NEUR-) NEURALAB LTD.

XX Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI; 2001-032104/04.

XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -

XX Disclosure; Figure 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.

XX Sequence 10 AA;

Query Match 90.0%; Score 9; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00067;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 HHQKLVFFA 9
 |||||
 DB 1 hhqklvffa 9

Search completed: July 18, 2002, 10:18:15
 Job time: 96 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sv model

Run on: July 18, 2002, 10:16:54 ; Search time 14.43 seconds
(without alignments)
66.590 Million cell updates/sec

Title: US-09-724-842-27
Perfect score: 10
Sequence: 1 HHQKLVFFAQ 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	90.0	42	2 PN0512	beta-amyloid prote
2	9	90.0	57	2 E60045	Alzheimer's diseas
3	9	90.0	57	2 F00045	Alzheimer's diseas
4	9	90.0	57	2 G60045	Alzheimer's diseas
5	9	90.0	57	2 D60045	Alzheimer's diseas
6	9	90.0	57	2 A60045	Alzheimer's diseas
7	9	90.0	57	2 B60045	Alzheimer's diseas
8	9	90.0	82	2 P00438	Alzheimer's diseas
9	9	90.0	695	1 A49795	Alzheimer's diseas
10	9	90.0	747	2 JH0773	Alzheimer's diseas
11	9	90.0	770	1 QRHU44	Alzheimer's diseas
12	8	80.0	33	2 S23094	Alzheimer's diseas
13	8	80.0	695	2 A27485	beta-amyloid prote
14	8	80.0	695	2 S00550	Alzheimer's diseas
15	6	60.0	115	2 A20523	Alzheimer's diseas
16	6	60.0	152	2 T06645	conserved hypothet
17	6	60.0	156	2 B47335	hypothetical prote
18	6	60.0	156	2 F85495	yacc protein - Esc
19	6	60.0	156	2 F90644	hypothetical prote
20	6	60.0	231	2 H85138	hypothetical prote
21	6	60.0	352	2 T48903	wax synthase [limp
22	6	60.0	428	2 T48008	hypothetical prote
23	6	60.0	512	2 C91268	transcription acti
24	6	60.0	512	2 C41968	transcription acti
25	6	60.0	512	2 A66109	transcription acti
26	6	60.0	590	2 F95853	probable phospholi
27	6	60.0	763	2 S31300	probable membrane
28	6	60.0	1016	2 S30236	genome polyprotein
29	6	60.0	4427	2 PN0637	polyketide synthas

30	5	50.0	29	2	C47719	T-cell receptor al
31	5	50.0	32	2	S67962	valine--trna ligas
32	5	50.0	66	2	AE3608	hypothetical prote
33	5	50.0	75	2	S35774	T-cell receptor al
34	5	50.0	80	2	F96787	protein T4012.7 (1
35	5	50.0	86	2	B44530	T-cell receptor al
36	5	50.0	91	2	H82370	conserved hypothet
37	5	50.0	98	2	C71560	probable chitr t2
38	5	50.0	106	2	I40737	T2 protein - Chlam
39	5	50.0	110	2	A24092	T-cell receptor al
40	5	50.0	112	2	A69268	hypothetical prote
41	5	50.0	113	4	I39320	T cell receptor al
42	5	50.0	119	2	AC0080	probable dihydrone
43	5	50.0	120	2	AE0892	dihydroneopterin a
44	5	50.0	123	1	H65093	probable dihydrone
45	5	50.0	123	2	E91121	probable kinase (1

ALIGNMENTS

RESULT 1

PN0512
beta-amyloid protein - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C:Accession: PN0512
R:Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohn
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A:Title: Receptor-mediated specific biological activity of a beta-amyloid protein fr
A:Reference number: PN0512; MUID:93290653
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SHI>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C:Keywords: alternative splicing; amyloid

Query Match 90.0%; Score 9; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 13 HHQKLVFFA 21

RESULT 2

E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in
A:Reference number: A60045; MUID:92017079
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
C:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 18 HHQKLVFFA 26

```

RESULT 3
P60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:q1895; PIDN:CAA39592.1; PID:g1896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 18 HHQKLVFFA 26

RESULT 4
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 18 HHQKLVFFA 26

RESULT 5
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

```

```

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 18 HHQKLVFFA 26

RESULT 6
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 18 HHQKLVFFA 26

RESULT 7
B60045
Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
C:Species: Ursus maritimus (polar bear)
C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: B60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: B60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56128; NID:g2165; PIDN:CAA39593.1; PID:g2166
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 90.0%; Score 9; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 18 HHQKLVFFA 26

RESULT 8
PQ0438
Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
C:Accession: PQ0438; C60045
R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
Biochem. Biophys. Res. Commun. 188, 905-911, 1992
A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precurs
A:Reference number: PQ0438; MUID:93075180

```

A:Accession: PQ0438
A:Molecule type: DNA
A:Residues: 1-82 <DAV>
A:Cross-references: GB:M83556; GB:M83657
R:Johnstone, E.M.; Chaney, M.O.; Norris, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079
A:Accession: C60045
A:Molecule type: mRNA
A:Residues: 12-68 <JOH>
A:Cross-references: EMBL:X56129
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 90.0%; Score 9; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 29 HHQKLVFFA 37
|||||

RESULT 9
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C:Species: Macaca fascicularis (crab-eating macaque)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A49795
R:Podlinsky, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
A:Reference number: A49795; MUID:91273117
A:Accession: A49795
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-695 <POD>
A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing

Query Match 90.0%; Score 9; DB 1; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 609 HHQKLVFFA 617
|||||

RESULT 10
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AAB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid
F:267-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 90.0%; Score 9; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 661 HHQKLVFFA 669
|||||

RESULT 11
QRH044
Alzheimer's disease amyloid beta protein precursor [validated] - human
N:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a in
N:Containing: amyloid beta protein long, plaque form; amyloid beta protein short, vasc
protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
C:Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39453; I39453; I59562;
4668; A28583; A29302; A60805; JLO038; S06121; A60355; A59011; A38384; S28076; S38252
R:Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Bayney, R.M.; Unterbeck, A.;
Nucleic Acids Res. 17, 517-522, 1989
A:Title: The Prec4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded
A:Reference number: S02260; MUID:89128427
A:Accession: S02260
A:Molecule type: DNA
A:Residues: 1-288, 'V', 365-770 <LEM1>
A:Cross-references: EMBL:X13466
A:Note: alternative splice form APP(695)
R:Lemaire, H.G.
Submitted to the EMBL Data Library, November 1988
A:Reference number: S05194
A:Accession: S05194
A:Molecule type: DNA
A:Residues: 1-14, 'V', 17-288, 'V', 365-770 <LEM2>
A:Cross-references: EMBL:X13466; NID:g35598; PIDN:CRAA31830.1; PID:g871360
R:La Fauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A:Title: Characterization of the 5'-end region and the first two exons of the beta-p
A:Reference number: A32277; MUID:89165870
A:Accession: A32277
A:Molecule type: DNA
A:Residues: 1-75 <LAF>
A:Cross-references: GB:M24546; GB:M24547; NID:g341202; PIDN:AAC13654.1; PID:g516074
R:Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A:Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows simil
A:Reference number: A33260; MUID:89392030
A:Accession: A33260
A:Molecule type: DNA
A:Residues: 656-737 <JOH>
A:Cross-references: GB:M29270; NID:g178863; PIDN:AAA51768.1; PID:g178865
R:Prelli, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione,
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A:Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid
A:Reference number: A35486; MUID:90321244
A:Accession: A35486
A:Molecule type: DNA
A:Residues: 672-710 <PRE1>
A:Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R:Yoshikai, S.I.; Sakaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A:Title: Genomic organization of the human amyloid beta-protein precursor gene.
A:Reference number: I39451; MUID:90236318
A:Accession: I39452
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB,
A:Molecule type: DNA
A:Residues: 1-770 <YOS1>
A:Cross-references: GB:M33112; NID:g178613; PIDN:AAB59502.1; PID:g178616
A:Accession: I39451
A>Status: nucleic acid sequence not shown; translation not shown; translated from GB,
A:Molecule type: DNA
A:Residues: 1-530, 'QWLMPVIPAFWEAKVGR' <YOS2>

A:Cross-references: GB:M34875; NID:g178608; PIDN:AA59501.1; PID:g178615
R:Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuya, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A:Reference number: A59020; MUID:91340168
A:Contents: annotation; erratum
A:Note: revised physical map for reference I39451
R:Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duine
Science 248, 1124-1126, 1990
A:Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A:Reference number: I39453; MUID:90260663
A:Accession: I39453
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 656-737 <LEV>
A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A:Note: a mutation with 693-Gln is presented
R:Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553
A:Accession: I59562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:557665; NID:g236720; PIDN:AA19991.1; PID:g236721
R:Kanino, K.; Ori, H.T.; Payami, H.; Wajzman, E.M.; Alonso, M.E.; Pulst, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAN>
A:Cross-references: GB:545135; NID:g257377; PIDN:AB23645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAN2>
A:Cross-references: GB:545136; NID:g257379; PIDN:AB23646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
A:Note: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1997
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(495)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular
A:Reference number: A29030; MUID:87231971
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th

A:Reference number: A47585; MUID:87120329
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dykes, T.; Weidemann, A.; Muthaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Mue
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 p
A:Reference number: S02638; MUID:88296437
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYK>
R:Tanzi, R.E.; McClatchey, A.I.; Lampert, E.D.; Villa-Komaroff, L.; Gusella, J.F.; N.
Nature 331, 528-530, 1988
A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A:Reference number: S00707; MUID:88122640
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
A:Reference number: S00925; MUID:88122639
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
A:Reference number: A38949; MUID:88122641
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A:Reference number: A30320
A:Accession: A30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Salim, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:88124954
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Muthaup, G.; Simms, G.; Pottgiesser, J.; Martins, R.N.; Beyreuther,
Query Match 90.0%; Score 9; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
 |||||
 Db 684 HHOKLVFFA 692

RESULT 12
 S23094
 beta-amyloid protein precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
 C:Accession: S23094
 R:Kojima, S.; Omori, M.
 FEBS Lett. 304, 57-60, 1992
 A:Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
 A:Reference number: S23094; MUID:92316198
 A:Accession: S23094
 A:Molecule type: protein
 A:Residues: 1-33 <KOJ>
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase

Query Match 80.0%; Score 8; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHOKLVFFA 9
 |||||
 Db 19 HHOKLVFFA 26

RESULT 13
 A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precursor
 A:Reference number: A27485; MUID:88106489
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>
 A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g305085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
 A:Reference number: S19727; MUID:92096458
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210 'G', 212-220 'S', 222-396 'A', 398-402 'T', 404-448 'A', 450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:Izumi, R.; Yamada, T.; Yoshikawa, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheimer's
 A:Reference number: I49485; MUID:92209998
 A:Accession: I49485
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>
 A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
 C:Genetics:
 A:Map position: 16C3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 80.0%; Score 8; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHOKLVFFA 9
 |||||
 Db 610 HHOKLVFFA 617

RESULT 14
 S00550
 Alzheimer's disease amyloid beta protein precursor - rat
 N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: S00550; A41245; A39820; S46251
 R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.
 EMBO J. 7, 1365-1370, 1988
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat
 A:Reference number: S00550; MUID:88312583
 A:Accession: S00550
 A:Molecule type: mRNA
 A:Residues: 1-695 <SHI>
 A:Cross-references: EMBL:X07648; NID:g55616; PIDN:CAA30488.1; PID:g55617
 R:Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
 Science 241, 223-226, 1988
 A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan c
 A:Reference number: A41245; MUID:88264430
 A:Accession: A41245
 A:Molecule type: protein
 A:Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
 A:Note: evidence for heparan sulfate attachment
 R:Hesse, L.; Behr, D.; Masters, C.L.; Multhaup, G.
 FEBS Lett. 349, 109-116, 1994
 A:Title: The beta-A4 amyloid precursor protein binding to copper.
 A:Reference number: S46251; MUID:94320627
 A:Contents: annotation; copper binding sites
 A:Note: rat peptides were isolated but not sequenced
 R:Potempa, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
 J. Biol. Chem. 266, 8464-8469, 1991
 A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat
 A:Reference number: A39820; MUID:91217087
 A:Accession: A39820
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 18-32 <POT>
 A:Experimental source: brain
 C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques i
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type protein
 C:Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
 F:625-648/Domain: transmembrane #status predicted <TMM>

Query Match 80.0%; Score 8; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HHOKLVFFA 9
 |||||
 Db 610 HHOKLVFFA 617

RESULT 15
 AE0523
 conserved hypothetical protein STY0189 [Imported] - Salmonella enterica subsp. enter
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Far
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica s
 A:Reference number: AB0502; PMID:11677608

A:Accession: AE0523
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD01325.1; PID:g16501453; GSPDB:GN00176
C:Genetics:
A:Gene: STY0189

Query Match 50.0%; Score 6; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 LVFFAQ 10
 |||||
DB 59 LVFFAQ 64

Search completed: July 18, 2002, 10:18:56
Job time: 122 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:17:44 ; Search time 10.33 seconds
(without alignments)
37.483 Million cell updates/sec

Title: US-09-724-842-27
Perfect score: 10
Sequence: 1 HHOKLVFFAQ 10

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	90.0	57	1 A4_PIG	Q2023 sus scrofa
2	9	90.0	57	1 A4_URSMA	Q29149 ursus marit
3	9	90.0	58	1 A4_CANFA	Q28280 canis fami
4	9	90.0	58	1 A4_RABIT	Q28748 oryctolagus
5	9	90.0	58	1 A4_SHEEP	Q28757 ovis aries
6	9	90.0	59	1 A4_BOVIN	Q28053 bos taurus
7	9	90.0	751	1 A4_SAISC	Q85241 samiri sci
8	9	90.0	770	1 A4_HUMAN	P05067 homo sapien
9	8	80.0	770	1 A4_MOUSE	P12023 mus musculu
10	8	80.0	770	1 A4_RAT	P08592 rattus norv
11	6	60.0	115	1 YACC_ECOLI	P23838 escherichia
12	6	60.0	321	1 CVF_GUTH	O78494 guillardia
13	6	60.0	417	1 O65A_DRONE	P29822 drosophila
14	6	60.0	512	1 CADC_ECOLI	P3890 escherichia
15	6	60.0	763	1 YNS1_YEAST	P42843 saccharomyc
16	6	60.0	3080	1 POLG_ZYMYC	P18479 z genome po
17	6	60.0	3083	1 POLG_ZYMYC	P36979 z genome po
18	6	60.0	4427	1 PKSL_BACSU	Q05470 bacillus su
19	5	50.0	80	1 APPL_ARATH	P30224 arabidopsis
20	5	50.0	112	1 Y145_ARCFU	Q30092 archaeoglob
21	5	50.0	118	1 FOLB_HAEIN	P46362 haemophilus
22	5	50.0	122	1 FOLB_ECOLI	P31055 escherichia
23	5	50.0	152	1 SODC_ZANAE	O65174 zantedeschia
24	5	50.0	191	1 YAFB_CAEEL	P52879 caenorhabdi
25	5	50.0	201	1 ALAG_RABIT	P52227 oryctolagus
26	5	50.0	203	1 CHPE_PSEAE	Q87005 pseudomonas
27	5	50.0	208	1 Y644_METJA	Q58060 methanococc
28	5	50.0	214	1 ACUB_BACSU	P39066 bacillus su
29	5	50.0	233	1 MTRP_HUMAN	Q15012 homo sapien
30	5	50.0	253	1 YTBQ_BACSU	P33560 bacillus su
31	5	50.0	258	1 MIP_CHLPN	Q927p3 chlamydia p
32	5	50.0	273	1 LACG_AGRRD	P29824 agrobacteri
33	5	50.0	284	1 LEP_PSEFL	P26844 pseudomonas

34	5	50.0	308	1 NOD1_RHIME	P03031 rhizobium m
35	5	50.0	332	1 C1B3_CAVPO	Q9qz20 cavia porce
36	5	50.0	334	1 Y293_BUCAI	P57380 buchnera ap
37	5	50.0	336	1 USG_AZOVI	P96199 azotobacter
38	5	50.0	380	1 FD3E_SOYBN	P48625 glycine max
39	5	50.0	416	1 TFXD_RHILT	P42726 rhizobium l
40	5	50.0	425	1 RAFB_ECOLI	P16552 escherichia
41	5	50.0	444	1 CYB_RHOSH	Q02761 rhodobacter
42	5	50.0	446	1 SR54_MYCGE	P47294 mycoplasma
43	5	50.0	453	1 ST24_YEAST	P47154 saccharomyc
44	5	50.0	472	1 C901_ARATH	Q81569 arabidopsis
45	5	50.0	496	1 C7D9_SOYBN	O81971 glycine max

ALIGNMENTS

RESULT 1
A4_PIG
ID A4_PIG STANDARD; PRT; 57 AA.
AC Q2023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; Pubmed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis."
RL Brain Res. Mol. Brain Res. 10:299-305 (1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; X56127; CAA39592.1; ..
DR HSSP; P05067; 1BA4
DR InterPro; IPR001868; A4_APP, PARTIAL.
DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
DR PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neurexin; Transmembrane.
FT CHAIN 1 1
FT DOMAIN <1 33 BETA-AMYLOID PROTEIN (POTENTIAL).
FT TRANSMEM 34 57 EXTRACELLULAR (POTENTIAL).
FT NON_TER 57 57 POTENTIAL.
SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 90.0%; Score 9; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 HHOKLVFFA 9

```
Db 18 HHQKLVFFA 26
|||||
RESULT 2
A4_URSM A STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;
-----
Query Match 90.0%; Score 9; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.00065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHQKLVFFA 9
| | | | |
Db 18 HHQKLVFFA 26
| | | | |
RESULT 3
A4_CANFA STANDARD; PRT; 58 AA.
AC Q28280;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56128; CAA39593.1; -
CC HSP; P05067; IAML.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D8EBA82DFA CRC64;
-----
Query Match 90.0%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHQKLVFFA 9
| | | | |
Db 19 HHQKLVFFA 27
| | | | |
RESULT 4
A4_RABIT STANDARD; PRT; 58 AA.
AC Q28748;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (Fragment).
GN APP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
CC G(O) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X56125; CAA39590.1; -
CC HSP; P05067; IBA4.
CC InterPro; IPR001868; A4_APP.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
CC Glycoprotein; Amyloid; Neurone; Transmembrane.
FT CHAIN 1 1 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
-----
Query Match 90.0%; Score 9; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHQKLVFFA 9
| | | | |
Db 19 HHQKLVFFA 27
| | | | |
```

Brain Res. Mol. Brain Res. 10:299-305(1991).
 -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).
 -!- SUBCELLULAR LOCATION: Type I membrane protein.
 -!- SIMILARITY: BELONGS TO THE APP FAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 EMBL; X56129; CAA39594.1; -
 HSSP; P05067; 1BM4.
 InterPro; IPR001868; A4_APP.
 PROSITE; PS00319; A4_EXTRA; PARTIAL.
 PROSITE; PS00320; A4_INTRA; PARTIAL.
 Glycoprotein; Amyloid; Neurone; Transmembrane.
 NON_TER 1 1
 CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 34 57 POTENTIAL.
 DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 NON_TER 58 58
 SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
 SQ
 Query Match 90.0%; Score 9; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFA 9
 Db 18 HHQKLVFFA 26
 |||||
 RESULT 5
 ID A4_SHEEP STANDARD; PRT; 58 AA.
 AC Q28757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 EMBL; X56124; CAA39589.1; -
 HSSP; P05067; 1BM4.
 InterPro; IPR001868; A4_APP.
 PROSITE; PS00319; A4_EXTRA; PARTIAL.
 PROSITE; PS00320; A4_INTRA; PARTIAL.
 Glycoprotein; Amyloid; Neurone; Transmembrane.

modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 EMBL; X56130; CAA39595.1; -
 HSSP; P05067; 1AML.
 InterPro; IPR001868; A4_APP.
 PROSITE; PS00319; A4_EXTRA; PARTIAL.
 PROSITE; PS00320; A4_INTRA; PARTIAL.
 Glycoprotein; Amyloid; Neurone; Transmembrane.
 NON_TER 1 1
 CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 TRANSMEM 34 57 POTENTIAL.
 DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).
 NON_TER 58 58
 SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;
 SQ

Query Match 90.0%; Score 9; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFA 9
 Db 18 HHQKLVFFA 26
 |||||
 RESULT 6
 ID A4_BOVIN STANDARD; PRT; 59 AA.
 AC Q28053;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis."
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

 EMBL; X56124; CAA39589.1; -
 HSSP; P05067; 1BM4.
 InterPro; IPR001868; A4_APP.
 PROSITE; PS00319; A4_EXTRA; PARTIAL.
 PROSITE; PS00320; A4_INTRA; PARTIAL.
 Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1
 FT CHAIN 7 49
 FT DOMAIN <1 34
 FT TRANSMEM 35 58
 FT DOMAIN 59 >59
 FT NON_TER 59 59
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 90.0%; Score 9; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.00066;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
 Db 19 HHQKLVFFA 27

RESULT 7
 A4_SAISC
 ID A4_SAISC STANDARD; PRT; 751 AA.
 AC Q95241;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
 GN APP.
 OS Saimiri sciureus (Common squirrel monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
 OX NCBI_TaxID=9521;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver, and Kidney;
 RX MEDLINE=96108492; PubMed=8532114;
 RA Levy E., Amorim A., Frangione B., Walker L.C.;
 RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy".
 RL Neurobiol. Aging 16:805-808(1995).
 CC -1- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; S81024; AAD14347.1; -
 CC HSSP; P05067; 1AAP.
 CC InterPro; IPR001868; A4_APP.
 CC InterPro; IPR002223; Kunitz_BPTI.
 CC Pfam; PF02177; A4_EXTRA; 1.
 CC Pfam; PF00014; Kunitz_BPTI; 1.
 CC PRINTS; PR00203; AMYLOIDA4.
 CC PRINTS; PR00759; BASICPTASE.
 CC SMART; SM00006; A4_EXTRA; 1.
 CC SMART; SM00131; KU; 1.
 CC PROSITE; PS00319; A4_EXTRA; 1.
 CC PROSITE; PS00320; A4_INTRA; 1.
 CC PROSITE; PS00280; BPTI_KUNITZ_1; 1.

DR PROSITE; PS50279; BPTI_KUNITZ_2; 1.
 KW Glycoprotein; Amyloid; Neurone; Transmembrane; Alternative splicing;
 KW Signal; Serine protease inhibitor.
 FT CHAIN 1 17
 FT SIGNAL 18 751
 FT CHAIN 653 695
 FT DOMAIN 18 680
 FT TRANSMEM 681 704
 FT DOMAIN 705 751
 FT DOMAIN 287 345
 FT SITE 740 743
 FT ACT_SITE 301 302
 FT DISULFID 291 341
 FT DISULFID 300 324
 FT DISULFID 316 337
 FT CARBOHYD 523 523
 FT CARBOHYD 552 552
 SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 90.0%; Score 9; DB 1; Length 751;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
 Db 665 HHQKLVFFA 673

RESULT 8
 A4_HUMAN
 ID A4_HUMAN STANDARD; PRT; 770 AA.
 AC P05067; P09000; Q16011;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APPI) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
 GN APP OR A4 OR CVAP OR ADL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=871144572; PubMed=2881207;
 RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
 RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor".
 RL Nature 325:733-736(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122639; PubMed=2893289;
 RA Ponte P., Gonzalez-Dewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
 RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors".
 RL Nature 331:525-527(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89128427; PubMed=2783775;
 RA Lemaire H.-G., Salbaum J.M., Multhaup G., Kang J., Bayne R.M., Unterbeck A., Beyreuther K., Mueller-Hill B.;
 RT "The preA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded by 16 exons".
 RL Nucleic Acids Res. 17:517-522(1989).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97263807; PubMed=9108164;
 RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,

- RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus.";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
RA SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE-88122640; PubMed-2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease.";
RL Nature 331:528-530(1988).
RN [6]
RA SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE-88122641; PubMed-2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity.";
RL Nature 331:530-532(1988).
RN [7]
RA SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE-87231971; PubMed-3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [8]
RA SEQUENCE OF 507-770 FROM N.A.
RX MEDLINE-88124954; PubMed-2893379;
RA Zain S.B., Salim M., Chou W.G., Sajdel-Sulkowska E.M., Majocha R.E.,
RA Marotta C.A.;
RT "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
RA SEQUENCE OF 672-681.
RX MEDLINE-88035004; PubMed-3312495;
RA Partridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtellotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels.";
RL J. Neurochem. 49:1394-1401(1987).
RN [10]
RA SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE-90236318; PubMed-2110105;
RA Yoshikai S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene.";
RL Gene 87:257-263(1990).
RN [11]
RA SEQUENCE OF 1-10 FROM N.A.
RX TISSUE=Liver;
RC MEDLINE-89016647; PubMed-3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide.";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
RA SEQUENCE OF 18-50.
RX MEDLINE-87250462; PubMed-3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts.";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
RA IDENTITY OF APP WITH NEVIN-II.
RX MEDLINE-89384866; PubMed-2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RT the Kunitz domain is protease nexin-II.";
- RL Nature 341:144-147(1989).
RN [14]
RA PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE-90211252; PubMed-1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor.";
RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
RA COMPLEX WITH G(O).
RX MEDLINE-93188965; PubMed-8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(O).";
RL Nature 362:75-79(1993).
RN [16]
RA X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE-99215582; PubMed-10201399;
RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein.";
RL Nat. Struct. Biol. 6:327-331(1999).
RN [17]
RA X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE-91104913; PubMed-2125487;
RA Hynes T.R., Randal M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor.";
RL Biochemistry 29:10018-10022(1990).
RN [18]
RA STRUCTURE BY NMR OF 289-344.
RX MEDLINE-92031488; PubMed-1718421;
RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayne R.M.,
RA Kamarek M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein.";
RL Biochemistry 30:10467-10478(1991).
RN [19]
RA STRUCTURE BY NMR OF 672-699.
RX MEDLINE-94281210; PubMed-7516706;
RA Talafous J., Marciniowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide.";
RL Biochemistry 33:7788-7796(1994).
RN [20]
RA STRUCTURE BY NMR OF 696-706.
RX MEDLINE-97128622; PubMed-8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment.";
RL Biochemistry 35:16094-16104(1996).
RN [21]
RA STRUCTURE BY NMR OF 672-711.
RX MEDLINE-98359783; PubMed-9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RT environment. Is the membrane-spanning domain where we think it is?";
RL Biochemistry 37:11064-11077(1998).
RN [22]
RA STRUCTURE BY NMR OF 672-699.
RX MEDLINE-20400066; PubMed-10940222;
RA Poulsen S.-A., Watson A.A., Craik D.J.;
RT "Solution structures in aqueous SDS micelles of two amyloid beta
RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
RT site.";
RL J. Struct. Biol. 130:142-152(2000).
RN [23]
RA STRUCTURE BY NMR OF 681-706.
RX MEDLINE-20400065; PubMed-10940221;

RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Magglio J.E., Lee J.P.;
 RA "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE-88296437; PubMed-2900137;
 RA Dykes T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 RN [24]
 RP QUERY MATCH 90.0%; Score 9; DB 1; Length 770;
 RP Best Local Similarity 100.0%; Pred. No. 0.0054;
 RP Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVEFA 9
 DB 684 HHQKLVEFA 692
 RESULT 9
 A4_MOUSE STANDARD; PRT; 770 AA.
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid:10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE-92096458; PubMed-1756177;
 RA de Strooper B., van Leuven F., van den Bergh H.;
 RT "The amyloid beta protein precursor or protease nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochem. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-88106489; PubMed-3322280;
 RA Yamada T., Sasaki H., Furiya H., Miyata T., Goto I., Sasaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISIONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN-CD-1; TISSUE-Placenta;
 RX MEDLINE-89345111; PubMed-2566710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus.";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]
 RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE-9209998; PubMed-1555768;
 RA Izumi R., Yamada T., Yoshikawa S.I., Sasaki H., Hattori M.,
 RA Sasaki Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]

RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE-Brain, and Kidney;
 RX MEDLINE-89149813; PubMed-2493350;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY, AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X59379; -; NOT ANNOTATED_CDS.
 CC EMBL: M18373; AAA37139.1; -;
 CC EMBL: X15210; BAA33280.1; -;
 CC EMBL: D10603; BAA01456.1; -;
 CC EMBL: M24397; AAA39929.1; -;
 CC PIR: A27485; A27485.
 CC PIR: S04855; S04855.
 CC PIR: S19727; S19727.
 CC HSP: P05067; 10CM.
 CC MGI: MGI:88059; App.
 CC InterPro: IPR001868; A4_APP.
 CC InterPro: IPR002223; Kunitz_BPTI.
 CC Pfam: PF02177; A4_EXTRA; 1.
 CC Pfam: PF00014; Kunitz_BPTI; 1.
 CC PRINTS: PR00203; AMYLOIDA4.
 CC PRINTS: PR00759; BASICPTASE.
 CC SMART: SM00006; A4_EXTRA; 1.
 CC SMART: SM00131; KU; 1.
 CC PROSITE: PS00319; A4_EXTRA; 1.
 CC PROSITE: PS00320; A4_INTRA; 1.
 CC PROSITE: PS00280; BPTI_KUNITZ_1; 1.
 CC PROSITE: PS0279; BPTI_KUNITZ_2; 1.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 CC Alternative splicing; Serine
 CC BY SIMILARITY.
 CC SIGNAL 1 17
 CC CHAIN 18 770
 CC ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 CC HOMOLOG.
 CC DOMAIN 18 699
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 700 723
 CC POTENTIAL.
 CC DOMAIN 724 770
 CC CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 673 715
 CC EQUIVALENT OF BETA-AMYLOID PROTEIN.
 CC DOMAIN 287 345
 CC BPTI/KUNITZ INHIBITOR.
 CC SITE 759 762
 CC CLATHRIN-BINDING (BY SIMILARITY).
 CC FT DISULFID 291 341
 CC BY SIMILARITY.
 CC FT DISULFID 300 324
 CC BY SIMILARITY.
 CC FT DISULFID 316 337
 CC BY SIMILARITY.
 CC FT CARBOHYD 542 542
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 571 571
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 289 289
 CC E -> V (IN ISOFORM APP(695)).
 CC FT VARSPLIC 290 364
 CC MISSING (IN ISOFORM APP(695)).
 CC FT VARSPLIC 346 380
 CC MISSING (IN ISOFORM APP(751)).
 CC SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAFA7A CRC64;
 SQ

```
Query Match      80.0%; Score 8; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQKLVFFA 9
Db 685 HQKLVFFA.692

RESULT 10
A4_RAT
ID A4_RAT STANDARD; PRT; 770 AA.
AC P08592;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog precursor
DE (Amyloidogenic glycoprotein) (AG).
GN APP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

[1]
SEQUENCE OF 1-289 AND 365-770 FROM N.A.
RP TISSUE-Liver;
RX MEDLINE=89183625; PubMed=2648331;
RA Kang J., Mueller-Hill B.;
RT "The sequence of the two extra exons in rat preA4.";
RL Nucleic Acids Res. 17:2130-2130(1989).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
CC WITH X11-ALPHA, BETA, AND GAMMA. THE SEQUENCE SPECIFIC
CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.

-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL; X07648; CAA30488.1; -
DR EMBL; X14066; CAA32229.1; -
DR PIR; S00550; S00550.
DR PIR; S03607; S03607.
DR HSP; P05067; IAAp.
DR InterPro; IPR001868; A4_APP.
DR InterPro; IPR002223; Kunitz_BPTI.
DR Pfam; PF02177; A4_EXTRA; 1.
DR Pfam; PF00014; Kunitz_BPTI; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00759; BASICPTASE.
DR SMART; SM00006; A4_EXTRA; 1.

SMART; SM00131; KU; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
KW Alternative splicing; Serine protease inhibitor.
FT SIGNAL 1 17
FT CHAIN 18 770
FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
FT HOMOLOG.
FT DOMAIN 18 699
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 700 723
FT POTENTIAL.
FT DOMAIN 724 770
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 673 715
FT EQUIVALENT OF BETA-AMYLOID PROTEIN.
FT DOMAIN 287 345
FT BPTI/KUNITZ INHIBITOR.
FT SITE 759 762
FT CLATHRIN-BINDING (BY SIMILARITY).
FT DISULFID 291 341
FT BY SIMILARITY.
FT DISULFID 300 324
FT BY SIMILARITY.
FT DISULFID 316 337
FT BY SIMILARITY.
FT CARBOHYD 542 542
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 571 571
FT N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPIC 289 289
FT E -> V (IN ISOFORM APP(695)).
FT VARSPIC 290 364
FT MISSING (IN ISOFORM APP(695)).
SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B2D929A7 CRC64;

Query Match      80.0%; Score 8; DB 1; Length 770;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HQKLVFFA 9
Db 685 HQKLVFFA.692

RESULT 11
YACC_ECOLI
ID YACC_ECOLI STANDARD; PRT; 115 AA.
AC P23838; P75654;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yacc precursor.
GN YACC OR B0122.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89327165; PubMed=2666401;
RA Xie Q.W., Tabor C.W., Tabor H.;
RT "Spermidine biosynthesis in Escherichia coli: promoter and
RT termination regions of the speed operon.";
RL J. Bacteriol. 171:4457-4465(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of
RT the 2.4-4.1 min (110,917-193,643 bp) region.";
RL Nucleic Acids Res. 22:1637-1639(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1233-1238(1997).
```



```

CC ----- This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J02804; AAA24642.1; -
DR EMBL: D26562; CAB20296.1; -
DR EMBL: AE000121; AAC73233.1; ALT_INIT.
DR PIR: A33863; A33863.
DR PIR: S45199; S45199.
DR EcoGene: EG11089; yacC.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 115 HYPOTHETICAL PROTEIN YACC.
SQ SEQUENCE 115 AA; 12854 MW; C078DD2653221EC9 CRC64;

Query Match 60.0%; Score 6; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LVFFAQ 10
DB 59 LVFFAQ 64
|||||
PRT; 321 AA.
AC O78494, STANDARD; PRT; 321 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apocytocrome F precursor.
GN PENA.
OS Guillardia theta (Cryptomonas phi).
OG Chloroplast.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99128221; PubMed=9929392;
RA Douglas S.E., Penny S.L.;
RT "The plastid genome of the cryptophyte alga, Guillardia theta:
RT complete sequence and conserved syntenic groups confirm its common
RT ancestry with red algae."
RL J. Mol. Evol. 48:236-244(1999).
CC -1- FUNCTION: TRANSLOCATES PROTONS ACROSS THE THYLAKOID MEMBRANE AND
CC TRANSFERS ELECTRONS FROM PHOTOSYSTEM II TO PHOTOSYSTEM I. IT
CC RECEIVES ELECTRONS FROM THE RIESKE IRON-SULFUR PROTEIN AND PASSES
CC THEM TO PLASTOCYANIN; THIS FUNCTION IS VERY SIMILAR TO THAT OF
CC MITOCHONDRIAL CYTOCHROME C1.
CC -1- SUBUNIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING
CC CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN.
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane (Probable).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C FAMILY.
CC -----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF041468; AAC35695.1; -
DR HSRP; P36438; IHCC2.
DR InterPro; IPR002325; Apocyt_F.
DR InterPro; IPR000345; CytC_heme_bind.

```

```

DR Pfam: PF01333; Apocytocrome_F; 1.
DR PRINTS: PR00610; CYTOCHROME_F.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme; Chloroplast; Thylakoid;
KW Photosynthesis; Photosystem I; Photosystem II; Transit peptide;
KW Transmembrane.
FT CHAIN 1 38 CHLOROPLAST (BY SIMILARITY).
FT TRANSIT 39 321 APOCYTOCHROME F.
FT BINDING 59 59 HEME (COVALENT) (PROBABLE).
FT BINDING 62 62 HEME (COVALENT) (PROBABLE).
FT METAL 63 63 IRON (HEME AXIAL LIGAND) (PROBABLE).
FT TRANSMEM 287 307 POTENTIAL.
SQ SEQUENCE 321 AA; 35173 MW; 42A1FF89FB05AE3D CRC64;

Query Match 60.0%; Score 6; DB 1; Length 321;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HOKLVF 7
DB 161 HOKLVF 166
|||||
PRT; 417 AA.
ID O65A_DROME STANDARD; PRT; 417 AA.
AC P82982;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative odorant receptor 65a.
GN OR65A.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reineb K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Rhne B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

```


RP SEQUENCE OF 149-763 FROM N.A.
 RA Maurer C.T.C., Urbanus J.H.M., Planta R.J.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: CONTAINS 1 F-BOX DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; 246259; CAA86384.1; -;
 DR EMBL; 271587; CAA96240.1; -;
 DR SGD; S0005255; YNL311C.
 DR InterPro; IPR001810; F-box.
 DR Pfam; PF00646; F-box; 1.
 DR SMART; SM00256; FBOX; 1.
 DR PROSITE; PS0181; FBOX; 1.
 DR KW Hypothetical protein.
 FT DOMAIN 54 100 F-BOX.
 FT DOMAIN 22 28 POLY-GLU.
 SQ SEQUENCE 763 AA; 88941 MW; 81102168449051BC CRC64;

Query Match 60.0%; Score 6; DB 1; Length 763;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLV 6
 |||||
 DB 323 HHQKLV 328

Search completed: July 18, 2002, 10:19:45
 Job time: 121 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:17:24 ; Search time 25.04 Seconds
(without alignments)
69.087 Million cell updates/sec

Title: US-09-724-842-27
Perfect score: 10
Sequence: 1 HHQKLVFFAQ 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL_19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	90.0	28	Q9UCD1	Q9UCD1 homo sapien
2	9	90.0	30	Q9UCA9	Q9UCA9 homo sapien
3	9	90.0	33	Q9UC33	Q9UC33 homo sapien
4	9	90.0	82	P78438	P78438 homo sapien
5	9	90.0	82	Q16014	Q16014 homo sapien
6	9	90.0	82	Q16019	Q16019 homo sapien
7	9	90.0	82	Q16020	Q16020 homo sapien
8	9	90.0	97	Q13778	Q13778 homo sapien
9	9	90.0	534	Q93296	Q93296 gallus gall
10	9	90.0	569	Q9PVL1	Q9PVL1 gallus gall
11	9	90.0	693	Q98SG0	Q98SG0 xenopus lae
12	9	90.0	695	Q95KN7	Q95KN7 macaca fasc
13	9	90.0	695	Q60496	Q60496 cavia sp. p
14	9	90.0	695	Q9DCJ8	Q9DCJ8 gallus gall
15	9	90.0	695	Q98SF9	Q98SF9 xenopus lae
16	9	90.0	747	Q91963	Q91963 xenopus. ap

17	9	90.0	751	13	Q9DGJ7	Q9DGJ7 gallus gall
18	9	90.0	770	6	Q9TUI0	Q9TUI0 sus scrofa
19	9	90.0	780	13	O73683	O73683 tetraodon f
20	8	80.0	79	11	O35463	O35463 cricetus
21	8	80.0	607	11	Q99K32	Q99K32 mus musculus
22	8	80.0	612	13	Q919E7	Q919E7 brachydanio
23	8	80.0	695	11	P97487	P97487 mus musculus
24	8	80.0	699	13	O57394	O57394 narke japon
25	8	80.0	737	13	O93279	O93279 fugu rubrip
26	8	80.0	738	13	Q90W28	Q90W28 brachydanio
27	7	70.0	19	4	Q9UCC8	Q9UCC8 homo sapien
28	6	60.0	152	10	Q9ST29	Q9ST29 arabidopsis
29	6	60.0	231	10	Q9SV79	Q9SV79 arabidopsis
30	6	60.0	352	10	Q9XGY6	Q9XGY6 simmondsia
31	6	60.0	428	10	Q9M108	Q9M108 arabidopsis
32	6	60.0	451	12	Q83329	Q83329 zucchini ye
33	6	60.0	574	17	Q9HJC7	Q9HJC7 thermoplasma
34	6	60.0	590	16	Q92X68	Q92X68 rhizobium m
35	6	60.0	623	5	Q9VBV8	Q9VBV8 drosophila
36	6	60.0	1016	12	O05912	O05912 zucchini ye
37	5	50.0	14	4	Q9UH91	Q9UH91 homo sapien
38	5	50.0	15	5	Q9TWF5	Q9TWF5 artemia (br
39	5	50.0	34	2	Q9ZG38	Q9ZG38 chlamydia t
40	5	50.0	34	8	Q9XQR5	Q9XQR5 pisum sativ
41	5	50.0	55	5	Q9NMJ6	Q9NMJ6 leishmania
42	5	50.0	91	16	Q9KVT2	Q9KVT2 vibrio chol
43	5	50.0	94	16	Q9AOW1	Q9AOW1 streptococc
44	5	50.0	98	16	O84083	O84083 chlamydia t
45	5	50.0	100	8	O99895	O99895 microathria

ALIGNMENTS

RESULT 1
Q9UCD1
ID Q9UCD1 PRELIMINARY; PRT; 28 AA.
AC Q9UCD1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94045685; PubMed=8229004;
RA Vingo-Pelfrey C., Lee D., Kelm P., Lieberburg I., Schenk D.B.;
RT "Characterization of beta-amyloid peptide from human cerebrospinal
RT fluid.";
RL J. Neurochem. 61:1965-1968(1993).
DR HSP; P05067; IAMB.
SQ SEQUENCE 28 AA; 3244 MW; DE7BD081160AFC81 CRC64;

Query Match 90.0%; Score 9; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 13 HHQKLVFFA 21

RESULT 2
Q9UCA9 PRELIMINARY; PRT; 30 AA.
ID Q9UCA9
AC Q9UCA9
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

```

DE BETA-AMYLOID PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94153015; PubMed=8109908;
RA Wisniewski T., Lalowski M., Levy E., Marques M.R., Frangione B.;
RT "The amino acid sequence of neuritic plaque amyloid from a familial
RT Alzheimer's disease patient.";
RL Ann. Neurol. 35:245-246(1994).
DR HSP; P05067; IBA4.
SQ SEQUENCE 30 AA; 3391 MW; FF4167ABD081160A CRC64;

Query Match 90.0%; Score 9; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 13 HHQKLVFFA 21

RESULT 3
Q9UC33 PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSP; P05067; IBA4.
SQ SEQUENCE 33 AA; 3674 MW; B1DEF2F4167ABD0 CRC64;

Query Match 90.0%; Score 9; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 13 HHQKLVFFA 21

RESULT 4
P78438 PRELIMINARY; PRT; 82 AA.
AC P78438;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE AMYLOID PROTEIN (BETA-AMYLOID PROTEIN) (FRAGMENT).
OS APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=89392030; PubMed=2675837;
RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
RA Little S.P.;
RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
RT similarity to soybean trypsin inhibitor.";
RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
RN [2]
RP SEQUENCE OF 19-48 FROM N.A.
RX MEDLINE=87120329; PubMed=2949367;
RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
RT linkage near the Alzheimer locus.";
RL Science 235:880-884(1987).
RN [3]
RP SEQUENCE OF 32-63 FROM N.A.
RX MEDLINE=93035397; PubMed=1415269;
RA Kamino K., Orr H.T., Payami H., Wijsman E.M., Alonso M.E., Pulst S.M.,
RA Anderson L., O'dahl S., Nemens E., White J.A.;
RT "Linkage and mutational analysis of familial Alzheimer disease
RT kindreds for the APP gene region.";
RL Am. J. Hum. Genet. 51:998-1014(1992).
DR EMBL; M29270; AAA51768.1; -
DR EMBL; M29269; AAA51768.1; JOINED.
DR EMBL; M15532; AAA51564.1; -
DR EMBL; S45136; AAB23646.1; -
DR HSP; P05067; IBA4.
FT NON_TER 1
SQ SEQUENCE 82 AA; 8994 MW; 8DA9B42B813A070E CRC64;

Query Match 90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 29 HHQKLVFFA 37

RESULT 5
Q16014 PRELIMINARY; PRT; 82 AA.
AC Q16014;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE BETA-AMYLOID PEPTIDE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenczwaig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL; S60721; AAB26263.2; -
DR HSP; P05067; IBA4.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 90.0%; Score 9; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
DB 30 HHQKLVFFA 38

```

RESULT 6
 Q16019 ID Q16019 PRELIMINARY; PRT; 82 AA.
 AC Q16019;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenczwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S61380; AAB26265.2;
 DR HSSP; P05067; 1BA4.
 DR NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 90.0%; Score 9; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFA 9
 Db 30 HHQKLVFFA 38
 |||||

RESULT 7
 Q16020 ID Q16020 PRELIMINARY; PRT; 82 AA.
 AC Q16020;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE BETA-AMYLOID PEPTIDE (FRAGMENT).
 GN BETA APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=93236601; PubMed=8476439;
 RA Denman R.B., Rosenczwaig R., Miller D.L.;
 RT "A system for studying the effect(s) of familial Alzheimer disease
 mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S61383; AAB26265.2;
 DR HSSP; P05067; 1BA4.
 DR NON_TER 1
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 90.0%; Score 9; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.0028;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFA 9
 Db 30 HHQKLVFFA 38
 |||||

RESULT 8
 Q13778 ID Q13778 PRELIMINARY; PRT; 97 AA.
 AC Q13778;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE AMYLOID PROTEIN (AD-AP) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=87120328; PubMed=3810169;
 RA Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
 RT "Characterization and chromosomal localization of a cDNA encoding
 the brain amyloid of Alzheimer's disease.";
 RL Science 235:877-880(1987).
 DR EMBL; M15533; AAA35540.1;
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE47AE CRC64;

Query Match 90.0%; Score 9; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFA 9
 Db 11 HHQKLVFFA 19
 |||||

RESULT 9
 Q93296 ID Q93296 PRELIMINARY; PRT; 534 AA.
 AC Q93296;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE AMYLOID PROTEIN (FRAGMENT).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98337885; PubMed=9671674;
 RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
 RA Milligan C.E.;
 RT "Increased production of amyloid precursor protein provides a
 substrate for caspase-3 in dying motoneurons.";
 RL J. Neurosci. 18:5889-5890(1998).
 DR EMBL; AF042098; AAC25052.1;
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 90.0%; Score 9; DB 13; Length 534;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HHQKLVFFA 9

```

Db 448 HHQKLVFFA 456
|||||
RESULT 10
Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID PROTEIN (FRAGMENT).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-(2000).
DR EMBL; AF030341; AAF12698.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.
DR NON_TER 1.
FT SEQUENCE 569 AA; 64753 MW; 0AB8BB851863A19D CRC64;
SQ

Query Match 90.0%; Score 9; DB 13; Length 569;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
|||||
Db 484 HHQKLVFFA 492

RESULT 11
Q98SG0 PRELIMINARY; PRT; 693 AA.
AC Q98SG0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BETA-AMYLOID PRECURSOR PROTEIN A.
GN APP.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Van den Hurk W.H.;
RL Thesis (2001), Department of Biological Sciences,
RL University of Nijmegen, Nijmegen, Netherlands.
DR EMBL; AJ298150; CAC37193.1; -.
DR HSSP; P05067; 1HZ3.
DR InterPro; IPR001868; A4_APP.
DR Pfam; PF02177; A4_EXTRA; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR SMART; SM00006; A4_EXTRA; 1.
DR PROSITE; PS00319; A4_EXTRA; 1.
DR PROSITE; PS00320; A4_INTRA; 1.

```

```

KW Signal. 18 POTENTIAL.
FT SIGNAL 1 18
SQ SEQUENCE 693 AA; 78568 MW; CAFIDF655CIAB653 CRC64;

Query Match 90.0%; Score 9; DB 13; Length 693;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
|||||
Db 607 HHQKLVFFA 615

RESULT 12
Q95KN7 PRELIMINARY; PRT; 695 AA.
ID Q95KN7;
AC Q95KN7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE AMYLOID B-PROTEIN PRECURSOR.
OC Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CEREBELLUM;
RX MEDLINE-91273117; PubMed-1905108;
RA Podlisy M.B., Tolan D.R., Selkoe D.J.;
RT "Homology of the amyloid beta protein precursor in monkey and human
RT supports a primate model for beta amyloidosis in Alzheimer's
RT disease.";
RL Am. J. Pathol. 138:1423-1435(1991).
DR EMBL; M58727; AAA36829.1; -.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 597 636 POTENTIAL.
SQ SEQUENCE 695 AA; 78663 MW; 4F6EA0139F969D56 CRC64;

Query Match 90.0%; Score 9; DB 6; Length 695;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
|||||
Db 609 HHQKLVFFA 617

RESULT 13
Q60496 PRELIMINARY; PRT; 695 AA.
ID Q60496;
AC Q60496;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE AMYLOID PRECURSOR PROTEIN.
OS Cavia sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10143;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE-97236426; PubMed-9116031;
RA Beck M., Mueller D., Bigl V.;
RT "Amyloid precursor protein in Guinea pigs - complete cDNA sequence and
RT alternative splicing.";
RL Biochim. Biophys. Acta 1351:17-21(1997).
DR EMBL; X97631; CAA66230.1; -.
DR HSSP; P05067; 1BA4.

```

DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 SQ SEQUENCE 695 AA; 78701 MW; 5196A0C4017F16AB CRC64;

Query Match 90.0%; Score 9; DB 11; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
 |||||

DB 609 HHOKLVFFA 617

RESULT 14

Q9DGJ8 PRELIMINARY; PRT; 695 AA.
 ID Q9DGJ8
 AC Q9DGJ8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN 695 ISOFORM.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID-9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sarasa M., Rodolose A., Sorribas V.;
 RT "Cloning of full-length chicken beta-amyloid precursor protein
 isoforms."
 * BL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF289218; ANG00593.1; -
 DR HSSP: P05067; IBA4.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 SQ SEQUENCE 695 AA; 78565 MW; F201ED02AEC86D95 CRC64;

Query Match 90.0%; Score 9; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
 |||||

DB 609 HHOKLVFFA 617

RESULT 15

Q98SF9 PRELIMINARY; PRT; 695 AA.
 ID Q98SF9
 AC Q98SF9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BETA-AMYLOID PRECURSOR PROTEIN B.
 GN APP.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID-8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van den Hurk W.H.;

RL Thesis (2001), Department of Biological Sciences,
 RL University of Nijmegen, Nijmegen, Netherlands.
 DR EMBL: AJ298151; CAC37194.1; -
 DR HSSP: P05067; IH23.
 DR InterPro: IPR001868; A4_APP.
 DR Pfam: PF02177; A4_EXTRA; 1.
 DR PRINTS: PR00203; AMYLOIDA4.
 DR SMART: SM00006; A4_EXTRA; 1.
 DR PROSITE: PS00319; A4_EXTRA; 1.
 DR PROSITE: PS00320; A4_INTRA; 1.
 KW Signal.
 FT SIGNAL 1 18 POTENTIAL.
 SQ SEQUENCE 695 AA; 78803 MW; DC14EB02AFB0204A CRC64;

Query Match 90.0%; Score 9; DB 13; Length 695;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFA 9
 |||||

DB 609 HHOKLVFFA 617

Search completed: July 18, 2002, 10:19:28
 Job time: 124 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2002, 10:16:49 ; Search time 12.97 Seconds
(without alignments)
18.832 Million cell updates/sec

Title: US-09-724-842-27
Perfect score: 10
Sequence: 1 HHQKLVFFAQ 10

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/prodata/2/1aa/5A_COMB.pep.*
2: /cgn2.6/prodata/2/1aa/5B_COMB.pep.*
3: /cgn2.6/prodata/2/1aa/6A_COMB.pep.*
4: /cgn2.6/prodata/2/1aa/6B_COMB.pep.*
5: /cgn2.6/prodata/2/1aa/PCTUS_COMB.pep.*
6: /cgn2.6/prodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	10	100.0	28	4	US-09-388-890-12	Sequence 12, Appl
2	10	100.0	40	1	US-08-304-585-8	Sequence 8, Appl
3	10	100.0	63	1	US-08-462-859A-3	Sequence 3, Appl
4	10	100.0	63	1	US-08-123-659A-3	Sequence 3, Appl
5	10	100.0	63	1	US-08-464-247A-3	Sequence 3, Appl
6	10	100.0	63	1	US-08-464-248A-3	Sequence 3, Appl
7	10	100.0	99	3	US-08-339-708A-6	Sequence 6, Appl
8	9	90.0	15	2	US-08-612-785B-37	Sequence 37, Appl
9	9	90.0	17	4	US-09-264-709A-2	Sequence 2, Appl
10	9	90.0	26	1	US-08-304-585-7	Sequence 7, Appl
11	9	90.0	28	1	US-08-346-849-4	Sequence 4, Appl
12	9	90.0	28	1	US-08-302-808-7	Sequence 7, Appl
13	9	90.0	28	2	US-08-609-090-2	Sequence 2, Appl
14	9	90.0	28	2	US-08-986-948-7	Sequence 7, Appl
15	9	90.0	28	2	US-08-293-284A-4	Sequence 4, Appl
16	9	90.0	28	2	US-08-461-216-2	Sequence 2, Appl
17	9	90.0	28	4	US-09-388-890-2	Sequence 2, Appl
18	9	90.0	28	4	US-09-388-890-3	Sequence 3, Appl
19	9	90.0	28	4	US-09-388-890-4	Sequence 4, Appl
20	9	90.0	28	4	US-09-388-890-5	Sequence 5, Appl
21	9	90.0	28	4	US-09-388-890-6	Sequence 6, Appl
22	9	90.0	28	4	US-09-388-890-7	Sequence 7, Appl
23	9	90.0	28	4	US-09-388-890-8	Sequence 8, Appl
24	9	90.0	28	4	US-09-388-890-13	Sequence 13, Appl
25	9	90.0	28	4	US-09-388-890-14	Sequence 14, Appl
26	9	90.0	28	4	US-09-264-709A-1	Sequence 1, Appl
27	9	90.0	28	4	US-08-723-661B-2	Sequence 2, Appl

28	9	90.0	30	2	US-08-609-090-3	Sequence 3, Appl
29	9	90.0	33	2	US-08-609-090-4	Sequence 4, Appl
30	9	90.0	35	1	US-08-304-585-6	Sequence 6, Appl
31	9	90.0	35	2	US-08-612-785B-36	Sequence 36, Appl
32	9	90.0	35	2	US-08-612-785B-38	Sequence 38, Appl
33	9	90.0	35	2	US-08-612-785B-40	Sequence 40, Appl
34	9	90.0	36	2	US-08-609-090-6	Sequence 6, Appl
35	9	90.0	38	1	US-08-302-808-1	Sequence 1, Appl
36	9	90.0	38	2	US-07-737-371E-68	Sequence 68, Appl
37	9	90.0	38	2	US-08-986-948-1	Sequence 1, Appl
38	9	90.0	39	1	US-08-304-585-5	Sequence 5, Appl
39	9	90.0	39	1	US-08-302-808-2	Sequence 2, Appl
40	9	90.0	39	2	US-08-609-090-7	Sequence 7, Appl
41	9	90.0	39	2	US-08-682-245A-1	Sequence 1, Appl
42	9	90.0	39	2	US-08-986-948-2	Sequence 2, Appl
43	9	90.0	40	1	US-07-744-767A-1	Sequence 1, Appl
44	9	90.0	40	1	US-08-235-400-2	Sequence 2, Appl
45	9	90.0	40	1	US-08-476-464A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-388-890-12
; Sequence 12, Application US/09388890
; Patent No. 6136548
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, STEPHEN
; TITLE OF INVENTION: METHODS FOR THE PREVENTION AND TREATMENT
; OF VASCULAR HEMORRHAGING AND ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWREY & SIMON
; STREET: 1299 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/388,890
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/686,959
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: AUERBACH, JEFFREY I.
; REGISTRATION NUMBER: 32,680
; TELEPHONE: (202) 383-7451
; TELEFAX: (202) 383-6610
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; IMMEDIATE SOURCE:
; CLONE: E22Q B(1-28) peptide of amyloid B protein
US-09-388-890-12

Query Match 100.0%; Score 10; DB 4; Length 28;

Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10
DB 13 HHQKLVEFFAQ 22

RESULT 2
US-08-304-585-8
; Sequence 8, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-304-585-8

Query Match 100.0%; Score 10; DB 1; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.le-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10
DB 13 HHQKLVEFFAQ 22

RESULT 3
US-08-462-859A-3
; Sequence 3, Application US/08462859A
; Patent No. 5652092
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5652092el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company

STREET: One Cyanamid Plaza
CITY: Wayne New Jersey
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 31,844-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)831-3246
; TELEFAX: (201)831-3305
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-859A-3

Query Match 100.0%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVEFFAQ 10
DB 22 HHQKLVEFFAQ 31

RESULT 4
US-08-123-659A-3
; Sequence 3, Application US/08123659A
; Patent No. 5656477
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vitek, M. P.
; TITLE OF INVENTION: No. 5656477el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; TITLE OF INVENTION: of B-Amyloid Peptide
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Anne Rosenblum
; STREET: 163 Delaware Avenue, Suite 212
; CITY: Delmar
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 12054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 20-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenblum, Anne M.
; REGISTRATION NUMBER: 30,419
; REFERENCE/DOCKET NUMBER: 31,844-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516)475-0611

TELEFAX: (518)475-0619
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-123-659A-3

Query Match 100.0%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
DB 22 HHOKLVFFAQ 31

RESULT 5

US-08-464-247A-3
; Sequence 3, Application US/08464247A
; Patent No. 5693478
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5693478el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,247A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2158
TELEFAX: 201-683-4117

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-247A-3

Query Match 100.0%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
DB 22 HHOKLVFFAQ 31

RESULT 6

US-08-464-248A-3
; Sequence 3, Application US/08464248A
; Patent No. 5703209
; GENERAL INFORMATION:
; APPLICANT: Jacobsen, J. S.
; APPLICANT: Vittek, M. P.
; TITLE OF INVENTION: No. 5703209el Amyloid Precursor and Method of
; TITLE OF INVENTION: Using Same to Access Agents Which Down-Regulate Formation
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,248A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,844-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)831-3246
TELEFAX: (201)831-3305

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-248A-3

Query Match 100.0%; Score 10; DB 1; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHOKLVFFAQ 10
DB 22 HHOKLVFFAQ 31

RESULT 7

US-08-339-708A-6
; Sequence 6, Application US/08339708A
; Patent No. 6037521
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiro
; APPLICANT: Takashi, Kobayashi
; APPLICANT: Tada, No. 6037521hiro
; APPLICANT: Shoji, Mikio
; APPLICANT: Kawarabayashi, Takeshi
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109

COMPUTER READABLE FORM:
US-08-339-708A-6

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,708A
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 306026/93
FILING DATE: 12-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: SANDERCOCK, COLIN G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 026083/0159
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-339-708A-6

Query Match 100.0%; Score 10; DB 3; Length 99;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHQKLVFFAQ 10
| | | | | | | | | |
Db 13 HHQKLVFFAQ 22

RESULT 8
US-08-612-785B-37
Sequence 37, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 90.0%; Score 9; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHQKLVFFA 9
| | | | | | | | | |
Db 3 HHQKLVFFA 11

RESULT 9
US-09-264-709A-2
Sequence 2, Application US/09264709A
Patent No. 6320024
GENERAL INFORMATION:
APPLICANT: Roberts, Eugene
TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
TITLE OF INVENTION: Improve the Quality of Life
FILE REFERENCE: 2124-310
CURRENT APPLICATION NUMBER: US/09/264,709A
CURRENT FILING DATE: 1999-03-09
PRIOR FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 2
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-09-264-709A-2

Query Match 90.0%; Score 9; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHQKLVFFA 9
| | | | | | | | | |
Db 2 HHQKLVFFA 10

RESULT 10
US-08-304-585-7
Sequence 7, Application US/08304585
Patent No. 5721106
GENERAL INFORMATION:
APPLICANT: Maggio, John E.
APPLICANT: Mantyh, Patrick W.
TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueeting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 561415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-304-585-7

Query Match 90.0%; Score 9; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HHQKLVFFA 9
Db 4 HHQKLVFFA 12

RESULT 11
US-08-346-849-4
; Sequence 4, Application US/08346849
; Patent No. 5670483
; GENERAL INFORMATION:
; APPLICANT: Zhang, Shuguang
; APPLICANT: Lockshin, Curtis
; APPLICANT: Rich, Alexander
; APPLICANT: Holmes, Todd
; TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
; TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
; THEREFOR
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173-4799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/346,849
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,326
; FILING DATE: 28 DECEMBER 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: MIT-6008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-346-849-4

Query Match 90.0%; Score 9; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
Db 13 HHQKLVFFA 21

RESULT 12
US-08-302-808-7
; Sequence 7, Application US/08302808
; Patent No. 5750349
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5750349uhiro
; APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/302,808
; FILING DATE: 15-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:
US-08-302-808-7

Query Match 90.0%; Score 9; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
| | | | | | | |
Db 13 HHQKLVFFA 21

RESULT 13
US-08-609-090-2
; Sequence 2, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124

INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-2

Query Match 90.0%; Score 9; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
| | | | | | | |
Db 13 HHQKLVFFA 21

RESULT 14
US-08-986-948-7
; Sequence 7, Application US/08986948
; Patent No. 5955317
; GENERAL INFORMATION:
; APPLICANT: SUZUKI, No. 5955317uhiro

APPLICANT: ODAKA, Asano
; APPLICANT: KITADA, Chieko
; TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
; DERIVATIVES AND USE THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIRE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02019

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,948
; FILING DATE:

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/302,808
; FILING DATE: 15-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00089
; FILING DATE: 24-JAN-1994
; APPLICATION NUMBER: 010132/1993
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: 019035/1993
; FILING DATE: 05-FEB-1993
; APPLICATION NUMBER: 286985/1993
; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993

ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-986-948-7

Query Match 90.0%; Score 9; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHQKLVFFA 9
| | | | | | | |
Db 13 HHQKLVFFA 21

RESULT 15
US-08-293-284A-4
; Sequence 4, Application US/08293284A
; Patent No. 5955343
; GENERAL INFORMATION:
; APPLICANT: Holmes, Todd
; APPLICANT: Zhang, Shuguang
; APPLICANT: Rich, Alexander

APPLICANT: Dipersio, C. Michael
APPLICANT: Lockshin, Curtis
TITLE OF INVENTION: STABLE MACROSCOPIC MEMBRANES FORMED BY
TITLE OF INVENTION: SELF-ASSEMBLY OF AMPHIPHILIC PEPTIDES AND USES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/293,284A
FILING DATE: 22-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,326
FILING DATE: 28-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: MIT-6008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-293-284A-4

Query Match 90.0%; Score 9; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHQKLVFFA 9
Db 13 HHQKLVFFA 21

Search completed: July 18, 2002, 10:18:35
Job time: 106 sec